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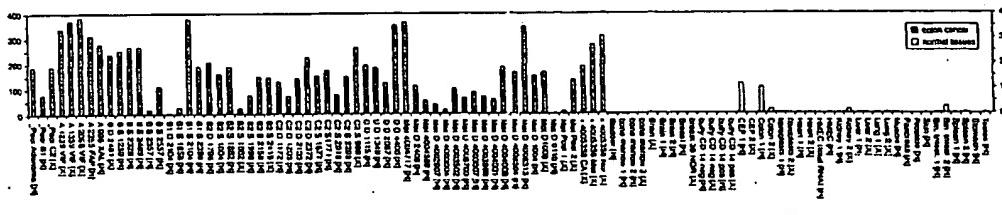
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(54) Title: METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS

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**NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND  
METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS**

**FIELD OF THE INVENTION**

The invention relates to the identification of expression profiles and the nucleic acids involved in colorectal cancer, and to the use of such expression profiles and nucleic acids in diagnosis and prognosis of colorectal cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate colorectal cancer.

**BACKGROUND OF THE INVENTION**

Colorectal cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- $\beta$  signaling pathway. For a review, see Molecular Biology of Colorectal Cancer, pp238-299, in Curr. Probl. Cancer, Sept/Oct 1997.

Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast

majority of colorectal cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

Thus, methods that can be used for diagnosis and prognosis of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of colorectal cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, provided herein are molecular targets for therapeutic intervention in colorectal and other cancers.

#### SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate colorectal cancer. Also provided herein are methods of inhibiting proliferation of cell, preferably a colorectal cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably colorectal cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided herein is a method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), the method comprising combining the CCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a CCMP. In one embodiment, the method comprises combining the CCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Also provided is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the CCMP, or an animal lacking the CCMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Furthermore, a method of diagnosing a disorder associated with colorectal cancer is provided. The method comprises determining the expression of a gene which encodes a colorectal cancer protein preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9 or a fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. A difference in the expression indicates that the first individual has a disorder associated with colorectal cancer.

In another aspect, the present invention provides an antibody which specifically binds to a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In a preferred embodiment, the fragment of CAA9 is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof. In a preferred embodiment, the method comprises combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof. The method further includes determining the binding of said CCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits colorectal cancer.

In a further aspect, a method for inhibiting colorectal cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment

thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting colorectal cancer is provided to an individual with cancer. As described herein, methods of inhibiting colorectal cancer can be performed by administering an inhibitor of colorectal cancer protein activity, including antisense molecules, and preferably small molecules.

Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

A method of neutralizing the effect of a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

In another aspect of the invention, a method of treating an individual for colorectal cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of CJA8. In another embodiment, the method comprises administering to a patient having colorectal cancer an antibody to CJA8 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

Also provided herein is a method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

#### DETAILED DESCRIPTION OF THE FIGURES

Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), upregulated in tumor tissue compared to normal colon tissue.

Figure 2 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 5 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 6 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 7 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 9 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 10 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 11 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 12 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 13 provides the Accession numbers for genes or fragments thereof, including descriptions of the gene or encoded protein, upregulated in tumor tissue compared to normal colon tissue.

Figure 14 provides a list of proteins, including Accession numbers for nucleic acid sequences associated with the encoding genes thereof, upregulated in tumor tissue compared to normal colon tissue.

Figure 15 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal protein provided herein, CAA2. The start and stop codon are shaded. The sequence within the two cross marks indicates a preferred novel fragment of CAA2 provided herein, referred to herein as the "CAA2 5' end". Preferred embodiments of CAA2 include at least a portion of the CAA2 5'. The sequence in bold and indicated with a bar at the bottom right beginning with "GGC" and ending with "AAA" can be found in Accession no. AA505133.

Figure 16 shows an embodiment of a nucleic acid encoding CAA2, wherein the start and stop codons are shaded.

Figure 17 shows an embodiment of an amino acid sequence of CAA2. Preferred fragments include at least about 10 amino acids in the N-terminal end. The N-terminus as defined herein includes an embodiment beginning at the first amino acid until about any one of the three amino acids marked with a dot above them. In another embodiment, the N-terminus of CAA2 is defined as the amino acid sequence encoded by the CAA2 5' end.

Figure 18 shows the amino acid sequence of CAA2p1, a preferred CAA2 fragment provided herein.

Figure 19 shows the amino acid sequence of CAA2p2, a preferred CAA2 fragment provided herein.

Figure 20 shows an alignment of the human and mouse CAA2 polypeptides provided herein. The mouse polypeptide contains at least some of the sequence of each of the following Accession numbers: AA386837; AI508773; AA505293; and AA636546.

Figure 21 shows the relative amount of expression of CAA2 in various samples of colon cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 22 shows an embodiment of a colorectal cancer nucleic acid, CAA9 mRNA. The start and stop codons are underlined.

Figure 23 shows the open reading frame of the CAA9 gene wherein the start and stop codons are underlined.

Figure 24 shows an embodiment of the amino acid sequence of a colorectal cancer protein, CAA9, wherein putative transmembrane sequences are underlined. In one embodiment, CAA9 or fragments

of CAA9 are soluble, therefore, the transmembrane domains are deleted, inactivated, and/or the peptide is truncated (with or without re-ligation) to form soluble CAA9.

Figure 25 shows embodiments of colorectal cancer proteins (also termed colorectal cancer modulator proteins). Specifically, Figure 25 shows CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS and their respective solubilities.

Figure 26 shows the relative amount of CAA9 expression in several different samples of colon cancer tissue (dark bars) and normal tissues (light bars).

Figure 27 shows the nucleic acid sequence for the gene encoding CGA7. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA331393. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 28A and 28B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 29 shows the amino acid sequence of CGA7.

Figures 30A and 30B show the relative expression of CGA7 in normal tissue and colon cancer tissue, respectively.

Figure 31 shows the nucleic acid sequence for the mRNA encoding CGA8. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA2786503. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 32A and 32B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 33 shows the amino acid sequence of CGA8.

Figure 34 shows the relative expression of CGA8 in breast cancer tissue, colon cancer tissue, normal tissue and fetal tissue.

Figure 35 shows the sequence for the mRNA encoding CJA8. Start (ATG) and stop (TAA) codons are indicated by shaded boxes.

Figure 36 shows the amino acid sequence for CJA8. A putative transmembrane region is designated by shading. A mouse homolog of this human protein is found at Accession Number AAF21308.1.

Figure 37 shows the relative amount of expression of CJA8 in several different samples of colon tissues (dark bars) and normal tissues (light bars).

Figure 38 shows the relative amount of expression of BCN7 in several different samples of colon tissues (dark bars) and normal tissues (light bars), as determined using the sequence of Accession Number N22107 as a probe.

Figure 39 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, BCN7.

Figure 40 shows the sequence for the mRNA encoding CZA8. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 41 shows the sequence for the mRNA encoding BCX2. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 42 shows the sequence for the mRNA encoding CBC2. Start (ATG) and stop (TAA) codons are indicated by underlining.

Figure 43 shows the sequence for the mRNA encoding CBC1. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 44 shows the sequence for the mRNA encoding CBC3. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 45 shows the sequence for the mRNA encoding BCN5. Start (ATG) and stop (TAA) codons are indicated by underlining.

Figure 46 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CJA9.

Figure 47 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA1.

Figure 48 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA2.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for colorectal cancer (CRC), as well as methods for screening for compositions which modulate CRC. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from CRC tissue, and within CRC tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of colon tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in CRC versus normal colon tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the CRC expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important CRC genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the CRC proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the CRC nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the CRC proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in colorectal cancer; CRC, herein termed "CRC sequences". As outlined below, CRC sequences include those that are up-regulated (i.e. expressed at a higher level) in CRC, as well as those that are down-regulated (i.e. expressed at a lower level) in CRC. In a preferred embodiment, the CRC sequences are from humans; however, as will be appreciated by those in the art, CRC sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other CRC sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). CRC sequences from other organisms may be obtained using the techniques outlined below.

CRC sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the CRC sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a CRC protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form

not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the CRC sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, CRC sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the CRC sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzi et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al., Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141-91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Bru et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., Angew. Chem. Int'l. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature ( $T_m$ ) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in  $T_m$  for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A CRC sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

The CRC sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are

commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the CRC screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, CRC sequences are those that are up-regulated in CRC; that is, the expression of these genes is higher in colorectal carcinoma as compared to normal colon tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

In a preferred embodiment, CRC sequences are those that are down-regulated in CRC; that is, the expression of these genes is lower in colorectal carcinoma as compared to normal colon tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

CRC proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the CRC protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or disregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the CRC sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid

sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

CRC proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In a preferred embodiment, the CRC proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an

endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. CRC proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

A CRC sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

As used herein, a nucleic acid is a "CRC nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably those represented in Figure 12, more preferably those represented in Figures 13A and 13B, still more preferably those of Figures 14-20, 22-25, 27-29, 31-33, 35-37 and 39-48, and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the

clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); <http://blast.wustl.edu/blast/ REACRCE.html>. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region: The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the sequences of the figures. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which encode the peptides identified in the figures, or their complements, are considered a CRC sequence. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al.,

both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, *supra*, and Tijssen, *supra*.

In addition, the CRC nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the CRC genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., *supra*, hereby expressly incorporated by reference.

Once the CRC nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire CRC nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant CRC nucleic acid can be further-used as a probe to identify and isolate other CRC nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant CRC nucleic acids and proteins.

The CRC nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the CRC nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene

therapy and/or antisense applications. Alternatively, the CRC nucleic acids that include coding regions of CRC proteins can be put into expression vectors for the expression of CRC proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to CRC nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the CRC nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent

binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic

acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

In a preferred embodiment, CRC nucleic acids encoding CRC proteins are used to make a variety of expression vectors to express CRC proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the CRC protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the

sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the CRC protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the CRC protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The CRC proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a CRC protein, under the appropriate conditions to

induce or cause expression of the CRC protein. The conditions appropriate for CRC protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeabacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

In a preferred embodiment, the CRC proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, CRC proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can

include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the CRC protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, CRC proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, CRC protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The CRC protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the CRC protein may be fused to a carrier protein to form an immunogen. Alternatively, the CRC protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the CRC protein is a CRC peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the CRC nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or

antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the CRC nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides CRC protein sequences. A CRC protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the CRC protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of CRC proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

CRC proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of CRC proteins are portions or fragments of the wild type sequences herein. In addition, as outlined above, the CRC

nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the CRC proteins are derivative or variant CRC proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative CRC peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the CRC peptide.

Also included in an embodiment of CRC proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the CRC protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant CRC protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the CRC protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed CRC variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of CRC protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the

molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the CRC protein are desired, substitutions are generally made in accordance with the following chart:

Original Residue	Chart I Exemplary Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the CRC proteins as needed. Alternatively, the variant may be designed such that the biological activity of the CRC protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of CRC polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a CRC polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a CRC polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking CRC to a water-insoluble support matrix or surface for use in the method for purifying anti-CRC antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the CRC polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence CRC polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence CRC polypeptide.

Addition of glycosylation sites to CRC polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence CRC polypeptide (for O-linked glycosylation sites). The CRC amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the CRC polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the CRC polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the CRC polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of CRC comprises linking the CRC polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

CRC polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a CRC polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a CRC polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the CRC polypeptide. The presence of such epitope-tagged forms of a CRC polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the CRC polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a CRC polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

Also included with the definition of CRC protein in one embodiment are other CRC proteins of the CRC family, and CRC proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related CRC proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the CRC nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, CRC proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

CRC proteins may also be identified as being encoded by CRC nucleic acids. Thus, CRC proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the CRC protein is to be used to generate antibodies, for example for immunotherapy, the CRC protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller CRC protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from CAA2p1 and CAA2p2. In another preferred embodiment, the epitope is selected from CAA9p1, CAA9p2, CAA9p3, CAAQ9p4, CAA9p4MAPS, CAA89p5 and CAA9p5MAPS.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab<sub>2</sub>, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the CAA2 or

fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include the CAA2 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a CRC protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to CRC are capable of reducing or eliminating the biological function of CRC, as is described below. That is, the addition of anti-CRC antibodies (either polyclonal or preferably monoclonal) to CRC (or cells containing CRC) may reduce or eliminate the CRC activity.

Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the CRC proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins; immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol.,

222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of CRC with an antibody raised against CRC proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the CRC proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted CRC protein.

In another preferred embodiment, the CRC protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the CRC protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane CRC protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the CRC protein. The antibody is also an antagonist of the CRC protein. Further, the antibody prevents activation of the transmembrane CRC protein. In one aspect, when the antibody prevents the binding of other molecules to the CRC protein, the antibody prevents growth of the cell. The antibody also sensitizes

the cell to cytotoxic agents, including, but not limited to TNF-a, TNF-b, IL-1, INF-g and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, CRC is treated by administering to a patient antibodies directed against the transmembrane CRC protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the CRC protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the CRC protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with CRC.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with CRC. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against CRC proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane CRC proteins not only serves to increase the local concentration of therapeutic moiety in the CRC afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the CRC protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the CRC protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The CRC antibodies of the invention specifically bind to CRC proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least  $10^4$ -  $10^6$  M<sup>-1</sup>, with a preferred range being  $10^7$  -  $10^9$  M<sup>-1</sup>.

In a preferred embodiment, the CRC protein is purified or isolated after expression. CRC proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the CRC protein may be purified using a standard anti-CRC antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., *Protein Purification*, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the CRC protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the CRC proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the CRC phenotype; that is, the expression levels of genes in normal colon tissue and in CRC tissue (and in some cases, for varying severities of CRC that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or CRC tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus CRC tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard

characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, *Nature Biotechnology*, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to CRC genes, i.e. those identified as being important in a CRC phenotype, can be evaluated in a CRC diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the CRC protein are detected. Although DNA or RNA encoding the CRC protein may be detected, of particular interest are methods wherein the mRNA encoding a CRC protein is detected. The presence of mRNA in a sample is an indication that the CRC gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled

nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a CRC protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, CRC proteins, including intracellular, transmembrane or secreted proteins, find use as markers of CRC. Detection of these proteins in putative CRC tissue or patients allows for a determination or diagnosis of CRC. Numerous methods known to those of ordinary skill in the art find use in detecting CRC. In one embodiment, antibodies are used to detect CRC proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the CRC protein is detected by immunoblotting with antibodies raised against the CRC protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the CRC protein find use in in situ imaging techniques. In this method cells are contacted with from one to many antibodies to the CRC protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the CRC protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of CRC proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing CRC from blood samples. As previously described, certain CRC proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted CRC proteins. Antibodies can be used to detect the CRC by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

In a preferred embodiment, in situ hybridization of labeled CRC nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including CRC tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

it is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to CRC severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the CRC probes are attached to biochips for the detection and quantification of CRC sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified CRC proteins are used in screening assays. That is, the present

invention provides novel methods for screening for compositions which modulate the CRC phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in CRC, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates colorectal cancer, modulates CRC proteins, binds to a CRC protein, or interferes between the binding of a CRC protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the CRC phenotype or the expression of a CRC sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a CRC phenotype, for example to a normal colon tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe CRC phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of a CRC protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random

chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of prokaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a

defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,

5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

The screens are done to identify drugs or bioactive agents that modulate the CRC phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in CRC similar to the expression profile of normal colon tissue is expected to result in a suppression of the CRC phenotype. Thus, in this embodiment, mimicking an expression profile, or changing one profile to another, is the goal.

In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the CRC phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a CRC expression pattern leading to a normal expression pattern, or modulate a single CRC gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated CRC tissue reveals genes that are not expressed in normal tissue or CRC tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for CRC genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated CRC tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of CRC cells, that thus has an associated CRC expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, CRC tissue may be screened for agents that reduce or suppress the CRC phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on CRC activity. By defining such a signature for the CRC phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "CRC proteins" or a "CCMP". In preferred embodiments, the CCMP is as depicted in Figures 17-20, 24, 25, 29, 33 and 36, more preferably the protein having the sequence shown in Figures 29 or 36 or encoded by the sequences of Figures 27, 36 and 39-48. The CCMP may be a fragment, or alternatively, be the full length protein to a fragment shown herein. Preferably, the CCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

In a preferred embodiment, the fragment is from CAA9. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the CAA9 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from CAA9p1, Caa9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

In a preferred embodiment, the fragment is charged and from the c-terminus of CAA2. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In another embodiment, the fragment is an internal peptide overlapping hydrophilic stretch of CAA2. In a preferred embodiment, the termini is blocked. Preferably, the fragment of CAA2 is selected from CAA2p1 or CAA2p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

In one embodiment the CRC proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the CRC protein is conjugated to BSA.

Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present.

Alternatively, cells comprising the CRC proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a CRC protein and a candidate bioactive agent, and determining the binding of the candidate agent to the CRC protein. Preferred embodiments utilize the human CRC protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative CRC proteins may be used.

Generally, in a preferred embodiment of the methods herein, the CRC protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the

composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the CRC protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the CRC protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the CRC protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labeled, and binding determined directly. For example, this may be done by attaching all or a portion of the CRC protein to a solid support, adding a labeled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using  $^{125}\text{I}$ , or with fluorophores. Alternatively, more than one component may be labeled with different labels; using  $^{125}\text{I}$  for the proteins, for example, and a fluorophor for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. CRC), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the CRC protein and thus is capable of binding to, and potentially modulating, the activity of the CRC protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the CRC protein with a higher affinity. Thus, if the candidate bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the CRC protein.

In a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the activity of the CRC proteins. In this embodiment, the methods comprise combining a CRC protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a CRC protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the CRC protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the CRC protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native CRC protein, but cannot bind to modified CRC proteins. The structure of the CRC protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect CRC bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of CRC proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of CRC proteins comprise the steps of adding a candidate bioactive agent to a sample of CRC proteins, as above, and determining an alteration in the biological activity of CRC proteins. "Modulating the activity of CRC" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to CRC proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of CRC proteins.

Thus, in this embodiment, the methods comprise combining a CRC sample and a candidate bioactive agent, and evaluating the effect on CRC activity. By "CRC activity" or grammatical equivalents herein is meant one of the CRC's biological activities, including, but not limited to, cell division, preferably in colon tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, CRC activity includes activation of CZA8, BCX2, CBC2, CBC1, CBC3, CJA9, BCN5, CQA1, BCN7, CQA2, CJA8,

CAA2, CAA9, CGA7 and/or CGA8\*, preferably one of the CRC proteins listed in Figure 14. An inhibitor of CRC activity is the inhibition of any one or more CRC activities.

In a preferred embodiment, the activity of the CRC protein is increased; in another preferred embodiment, the activity of the CRC protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a CRC protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising CRC proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a CRC protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the CRC protein. In one embodiment, "colorectal cancer protein activity" as used herein includes at least one of the following: colorectal cancer activity, binding to CJA8, activation of CJA8 or activation of substrates of CJA8 by CJA8. In one embodiment, colorectal cancer activity is defined as the unregulated proliferation of colon tissue, or the growth of cancer in colon tissue. In one aspect, colorectal cancer activity as defined herein is related to the activity of CJA8 in the upregulation of CJA8 in colon cancer tissue.

In another embodiment, colorectal cancer protein activity includes at least one of the following: colorectal cancer activity, binding to one of CAA2, CAA9, CGA7 and CGA8, activation of one of CAA2, CAA9, CGA7, and CGA8 or activation of substrates of CAA2, CAA9, CGA7 or CGA8 by CAA2, CAA9, CGA7 or CGA8, respectively. In one preferred embodiment, CAA2 comprises its N-terminal end. In one aspect, colorectal cancer activity as defined herein is related to the activity of CAA2, CAA9, CGA7 and/or CGA8 in the upregulation of CAA2, CAA9, CGA7 and/or CGA8, respectively, in colon cancer tissue.

In one embodiment, a method of inhibiting colon cancer cell division is provided. The method comprises administration of a colorectal cancer inhibitor.

In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a colorectal cancer inhibitor.

In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a colorectal cancer inhibitor.

In one embodiment, a colorectal cancer inhibitor is an antibody as discussed above. In another embodiment, the colorectal cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for colorectal cancer molecules. A preferred antisense molecule is for CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, BCN5, CQA1, BCN7, CQA2, CAA2, CAA9, CGA7 or CGA8, more preferably for the CRC sequences referenced in Figure 14, or for a ligand or activator thereof. A most preferred antisense molecule is for CJA8 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of

ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc.<sup>1</sup> Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various CRC sequences are important in CRC. Accordingly, disorders based on mutant or variant CRC genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant CRC genes comprising determining all or part of the sequence of at least one endogenous CRC genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the CRC genotype of an individual comprising determining all or part of the sequence of at least one CRC gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced CRC gene to a known CRC gene, i.e. a wild-type gene.

The sequence of all or part of the CRC gene can then be compared to the sequence of a known CRC gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the CRC gene of the patient and the known CRC gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the CRC genes are used as probes to determine the number of copies of the CRC gene in the genome.

In another preferred embodiment CRC genes are used as probed to determine the chromosomal localization of the CRC genes. Information such as chromosomal localization finds use in providing a

diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in CRC gene loci.

Thus, in one embodiment, methods of modulating CRC in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-CRC antibody that reduces or eliminates the biological activity of an endogenous CRC protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a CRC protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the CRC sequence is down-regulated in CRC, the activity of the CRC gene is increased by increasing the amount of CRC in the cell, for example by overexpressing the endogenous CRC or by administering a gene encoding the CRC sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the endogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the CRC sequence is up-regulated in CRC, the activity of the endogenous CRC gene is decreased, for example by the administration of a CRC antisense nucleic acid.

In one embodiment, the CRC proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to CRC proteins, which are useful as described herein. Similarly, the CRC proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify CRC antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a CRC protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the CRC antibodies may be coupled to standard affinity chromatography columns and used to purify CRC proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the CRC protein.

In one embodiment, a therapeutically effective dose of a CRC or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for CRC degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

The administration of the CRC proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the CRC proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a CRC protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, CRC proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, CRC genes (including both the full-length

sequence, partial sequences, or regulatory sequences of the CRC coding regions) can be administered in gene therapy applications, as is known in the art. These CRC genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

In a preferred embodiment, CRC genes are administered as DNA vaccines, either single genes or combinations of CRC genes. Naked DNA vaccines are generally known in the art. Brower, *Nature Biotechnology*, 16:1304-1305 (1998).

In one embodiment, CRC genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a CRC gene or portion of a CRC gene under the control of a promoter for expression in a CRC patient. The CRC gene used for DNA vaccines can encode full-length CRC proteins, but more preferably encodes portions of the CRC proteins including peptides derived from the CRC protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a CRC gene. Similarly, it is possible to immunize a patient with a plurality of CRC genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing CRC proteins.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the CRC polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

In another preferred embodiment CRC genes find use in generating animal models of CRC. As is appreciated by one of ordinary skill in the art, when the CRC gene identified is repressed or diminished in CRC tissue, gene therapy technology wherein antisense RNA directed to the CRC gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of CRC that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CRC protein. When desired, tissue-specific expression or knockout of the CRC protein may be necessary.

It is also possible that the CRC protein is overexpressed in CRC. As such, transgenic animals can be generated that overexpress the CRC protein. Depending on the desired expression level, promoters

of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CRC and are additionally useful in screening for bioactive molecules to treat CRC.

It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

## EXAMPLES

### Example 1

#### Tissue Preparation, Labeling Chips, and Fingerprints

##### Purify total RNA from tissue using TRIzol Reagent

Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.

#### HOMOGENIZATION

Before using generator, it should have been cleaned after last usage by running it through soapy H<sub>2</sub>O and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.

Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.

#### PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.

Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.

Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.

Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

#### RNA PRECIPITATION

Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

#### RNA WASH

Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C.

Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H<sub>2</sub>O. Try for 2-5ug/ul. Take absorbance readings.

#### Purify poly A+ mRNA from total RNA or clean up total RNA with Qiagen's RNeasy kit

Purification of poly A<sup>+</sup> mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.

Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A<sup>+</sup> mRNA has occurred.

Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

Read absorbance, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA must be precipitated.

Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

#### Ethanol Precipitation

Add 0.4 vol. of 7.5 M NH<sub>4</sub>OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash pellet with 0.5ml of 80%ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood. (Do not speed vacuum). Suspend pellet in DEPC H<sub>2</sub>O at 1ug/ul concentration.

#### Clean up total RNA using Qiagen's RNeasy kit

Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again.

Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution.

Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

#### Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

##### First Strand cDNA Synthesis

Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1<sup>st</sup> Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT. Incubate at 37C for 1 hour.

#### Second Strand Synthesis

Place 1<sup>st</sup> strand reactions on ice.

Add: 91ul DEPC H2O  
30ul 5X 2<sup>nd</sup> Strand Buffer  
3ul 10mM dNTP mix  
1ul 10U/ul *E.coli* DNA Ligase  
4ul 10U/ul *E.coli* DNA Polymerase  
1ul 2U/ul RNase H

Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C.

Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

#### Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes:  
Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH4Oac and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

#### In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

#### Make NTP labeling mix:

Combine at room temperature: 2ul T7 10xATP (75mM) (Ambion)  
2ul T7 10xGTP (75mM) (Ambion)  
1.5ul T7 10xCTP (75mM) (Ambion)

1.5ul T7 10xUTP (75mM) (Ambion)  
3.75ul 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or  
Enzo)  
3.75ul 10mM Bio-16-CTP (Enzo)  
2ul 10x T7 transcription buffer (Ambion)  
2ul 10x T7 enzyme mix (Ambion)

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

#### RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

#### Fragmentation

15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

#### 5 x Fragmentation buffer:

200 mM Tris-acetate, pH 8.1

500 mM KOAc

150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

#### Hybridization

200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

Hybridization Mix: fragment labeled RNA (50ng/ul final conc.)

50 pM 948-b control oligo  
1.5 pM BioB  
5 pM BioC  
25 pM BioD  
100 pM CRE  
0.1mg/ml herring sperm DNA  
0.5mg/ml acetylated BSA  
to 300 ul with 1xMES hyb. buffer

The instruction manuals for the products used herein are incorporated herein in their entirety.

Labeling Protocol Provided Herein

Hybridization reaction:

Start with non-biotinylated IVT (purified by RNeasy columns)

(ccc example 1 for steps from tissue to IVT)

IVT antisense RNA; 4 µg:           µl.

Random Hexamers (1 µg/µl):   4 µl

H<sub>2</sub>O:                                 µl

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14 µl

- Incubate 70°C, 10 min. Put on ice.

Reverse transcription:

5X First Strand (BRL) buffer: 6 µl

0.1 M DTT:                           3 µl

50X dNTP mix:                      0.6 µl

H<sub>2</sub>O:                                 2.4 µl

Cy3 or Cy5 dUTP (1mM):   3 µl

SS RT II (BRL):                   1 µl

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16 µl

- Add to hybridization reaction.

- Incubate 30 min., 42°C.

- Add 1 µl SSII and let go for another hour.

Put on ice.

- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H<sub>2</sub>O. dNTPs from Pharmacia)

**RNA degradation:**

	86.µl H <sub>2</sub> O
- Add 1.5 µl 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min.	10 µl 10N NaOH
	4 µl 50mM EDTA

**U-Con 30**

500 µl TE/sample spin at 7000g for 10 min, save flow through for purification

**Qiagen purification:**

- suspend u-con recovered material in 500µl buffer PB
- proceed w/ normal Qiagen protocol

**DNAse digest:**

- Add 1 µl of 1/100 dil of DNAse/30µl Rx and incubate at 37°C for 15 min.
- 5 min 95°C to denature enzyme

**Sample preparation:**

**- Add:**

Cot-1 DNA: 10 µl
50X dNTPs: 1 µl
20X SSC: 2.3 µl
Na pyro phosphate: 7.5 µl

10mg/ml Herring sperm DNA	1ul of 1/10 dilution
	21.8 final vol.

- Dry down in speed vac.
- Resuspend in 15 µl H<sub>2</sub>O.
- Add 0.38 µl 10% SDS.
- Heat 95°C, 2 min.
- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

**Washing after the hybridization:**

3X SSC/0.03% SDS:	2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H <sub>2</sub> O
1X SSC: 5 min.	12.5 mls 20X SSC in 250mls H <sub>2</sub> O

0.2X SSC: 5 min.                    2.5 mls 20X SSC in 250mls H<sub>2</sub>O

Dry slides in centrifuge, 1000 RPM, 1min.

Scan at appropriate PMT's and channels.

The results are shown in Figures 1 through 11. The lists of genes come from colorectal tumors from a variety of stages of the disease. The genes that are up regulated in the tumors (overall) were also found to be expressed at a limited amount or not at all in the body map. The body map for the colorectal project consists of ten tissues: Heart, Brain, Lung, Liver, Breast, Kidney, Prostate, Small Intestine, Spleen, and Colon. The down regulated genes in tumors (overall) versus normal colon were not selected for their expression or lack of expression in the body map. As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length. Figure 1 shows 51 upregulated genes; Figure 2 shows 194 upregulated genes; Figure 3 shows 1144 upregulated genes and Figure 4 shows 1815 upregulated genes. The genes shown in Figures 1 and 5 are particularly preferred. Figure 5 shows 54 downregulated genes; Figure 6 shows 558 downregulated genes; and Figure 7 shows 1923 downregulated genes; and Figures 8, 9, 10 and 11 provide the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

#### Example 2

Expression studies were performed herein.

As indicated in Figure 21, CAA2 is upregulated in colon cancer tissue. CAA2 is found in chromosome 15, cytoband 15q15-22, interval D15S146-D15S117. CAA2 has N-myristylation sites and a C-terminal microbody targeting signal. The preferred fragments shown in Figures 18 and 19 have a solubility of 1 mg/ 1 ml H<sub>2</sub>O.

As indicated in Figure 26, CAA9 is upregulated in colon cancer tissue. CAA9 is found in chromosome 5, cytoband 5q23.3, interval D5S471-D5S393.

As indicated in Figures 30A and 30B, CGA7 is upregulated in colon cancer tissue. CGA7 is found in chromosome 2.

As indicated in Figure 34, CGA8 is upregulated in colon cancer tissue.

As indicated in Figure 37, CJA8 is upregulated in colon cancer tissue. CJA8 is found in chromosome 11.

As indicated in Figure 38, BCN7 is upregulated in colon cancer tissue. BCN7 is found in chromosome 5, cytoband 5q22, interval D5S471-D5S393.

## CLAIMS

We claim:

1. A method of screening drug candidates comprising:
  - a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7 and CQA2 or a fragment thereof;
  - b) adding a drug candidate to said cell; and
  - c) determining the effect of said drug candidate on the expression of said expression profile gene.
2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.
3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.
4. A method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said CCMP.
5. A method for screening for a bioactive agent capable of modulating the activity of a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said CCMP.
6. A method of evaluating the effect of a candidate colorectal cancer drug comprising:
  - a) administering said drug to a patient;
  - b) removing a cell sample from said patient; and
  - c) determining the expression profile of said cell.
7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

8. A biochip comprising a nucleic acid segment encoding CJA81 or a fragment thereof; wherein said biochip comprises fewer than 1000 nucleic acid probes.
9. A method of diagnosing colorectal cancer comprising:
  - a) determining the expression of a gene encoding CJA8 or a fragment thereof in a first tissue type of a first individual; and
  - b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;wherein a difference in said expression indicates that the first individual has colorectal cancer.
10. An antibody which specifically binds to CJA8, or a fragment thereof.
11. An antibody which specifically binds to CAA9, or a fragment thereof.
12. The antibody of Claim 11 wherein said fragment is selected from the group CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.
13. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.
14. The antibody of Claim 10, wherein said antibody is a humanized antibody.
15. The antibody of Claim 10, wherein said antibody is an antibody fragment.
16. A method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer modulator protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof, said method comprising:
  - a) combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof; and
  - b) determining the binding of said CCMP or fragment thereof and said antibody.
17. A method for inhibiting colorectal cancer, said method comprising administering to a cell a composition comprising an antibody to CAJ8 or a fragment thereof.
18. The method of Claim 17 wherein said cell is a cell of an individual.
19. The method of Claim 18 wherein said individual has cancer.

20. The method of Claim 17 wherein said antibody is a humanized antibody.
21. The method of Claim 17 wherein said antibody is an antibody fragment.
22. A method for inhibiting colorectal cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to CJA8.
23. A peptide consisting essentially of CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 or CAA9p5MAPS.
24. A composition comprising the peptide of Claim 23.
25. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising CJA8 or a fragment thereof.
26. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof.
27. A composition capable of eliciting an immune response in an individual, said composition comprising CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
28. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
29. A method of treating an individual for colorectal cancer comprising administering to said individual an inhibitor of CJA8.
30. The method of Claim 29 wherein said inhibitor is an antibody.
31. A method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

32. A method of neutralizing the effect of a CJA8, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.
33. A method for localizing a therapeutic moiety to colorectal cancer tissue comprising exposing said tissue to an antibody to CJA8 or fragment thereof conjugated to said therapeutic moiety.
34. The method of Claim 33, wherein said therapeutic moiety is a cytotoxic agent.
35. The method of Claim 33, wherein said therapeutic moiety is a radioisotope.
36. A method of treating colorectal cancer comprising administering to an individual having colorectal cancer an antibody to CJA8 or fragment thereof conjugated to a therapeutic moiety.
37. The method of Claim 36, wherein said therapeutic moiety is a cytotoxic agent.
38. The method of Claim 36, wherein said therapeutic moiety is a radioisotope.

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PRIMARY KEY	FOLD UPREGULATED IN TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37677	>10	AA460530	Hs.98384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
6449	>10	X89986	Hs.32936	H.sapiens mRNA for NBK apoptotic inducer protein
4178	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
18330	>10	AA216722	Hs.54481	Human mRNA for apolipoprotein E receptor 2 complete cds
5692	>10	X17644	Hs.2707	G1 to S phase transition 1
16810	>10	AA053636	Hs.128849	PBK1 Human mRNA for KIAA0389 gene complete cds
33109	>10	W59961	Hs.22564	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds
37246	>10	AA449311	Hs.986558	mRNA complete cds
2857	>10	M58597	Hs.2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific) ESTs Weakly similar to ORF YPL212c [S.cerevisiae]
14338	>10	AA598712	Hs.23723	Homo sapiens human gamma-glutamyl hydrolase (hGH)
4676	9.6	U55206	Hs.78619	mRNA complete cds
2192	7.8	L48211	Hs.20954	Homo Sapiens angiotensin II receptor gene complete cds CDC28 protein kinase 2
5793	7.4	X54942	Hs.83758	Human mRNA for KIAA0096 gene partial cds
18231	6.3	AA199747	Hs.79025	Glutathione peroxidase 2 gastrointestinal ESTs Weakly similar to MOESINE/ZRIN/RADIXIN HOMOLOG [D.melanogaster]
6061	6.1	X68314	Hs.2704	
27117	5.0	AA405098	Hs.38178	
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds EST - HG2981-HT3127
1106	4.8	HG2981-HT3127	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
2157	4.6	L41939		

FIG.- 1Aa

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PRIMARY KEY	FOLD UPREGULATED IN TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
13193	4.4	AA442763	Hs.20483	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]
5690	4.4	X17620 AA479139 U48807	Hs.118638 Hs.75393 Hs.2359	NUCLEOSIDE DIPHOSPHATE KINASE A Acid phosphatase 1 soluble Human MAP kinase phosphatase (MKP-2) mRNA complete cds
28050	4.1			
4540	3.5			
26105	3.1	AA243133	Hs.48915	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds
19177	3.1	H10984 X54489 W93943	Hs.12338 Hs.789 Hs.59509	ESTs GRO1 oncogene (melanoma growth stimulating activity alpha) ESTs
5780	3.1			
33620	3.0	U48705 X62048	Hs.75562 Hs.75188	Receptor protein-tyrosine kinase EDDR1 WEE1-LIKE PROTEIN KINASE
4536	2.9			
5928	2.8	AA505133 R09195 AA453159	Hs.62273 Hs.151385 Hs.41723	ESTs Homo sapiens mRNA for KIAA0564 protein partial cds Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
28258	2.7			
21256	2.5			
27748	2.5			
25310	2.4	AA046745 M30448 U12595	Hs.110457 EST - M30448 Hs.2204	ESTs Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds
2640	2.4			
3834	2.3			
4674	2.3	U54999 X53800 AA011134	Hs.93121 Hs.89643 Hs.25863	Human LGN protein mRNA complete cds GRO3 oncogene ESTs Weakly similar to renin [H.sapiens]
5769	2.3			
25050	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
41935	2.3	AA292765	Hs.42650	H.sapiens mRNA for M-phase phosphoprotein mp5
26895	2.3	L12711	Hs.89643	Transketolase (Wernicke-Korsakoff syndrome)
1782	2.1			

FIG.- 1Ab

PRIMARY KEY	FOLD UPREGULATED IN TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25593	2.1	AA113149		Homo sapiens IPL (IPL) mRNA complete cds
1487	1.8	J03934		NAD(P)H:menadione oxidoreductase
7656	1.5	AA203428		ESTs Moderately similar to ANKYRIN BRAIN VARIANT 2 [Homo sapiens]
683	1.5	D79997		Human mRNA for KIAA0175 gene complete cds
836	1.5	D87444		Human mRNA for KIAA0255 gene complete cds
3098	1.2	M77836		PYRROLINE-5-CARBOXYLATE REDUCTASE
6879	1.1	Z29066		H.sapiens nek2 mRNA for protein kinase
6880	1.0	Z29067		H.sapiens nek3 mRNA for protein kinase
2473	0.7	M21904		Antigen identified by monoclonal antibodies 4F2 TRA1.10 TROP4 and T43
36508	0.7	AA429621		Human 100 kDa coactivator mRNA complete cds

*FIG.- 1Ac*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33616	>10	W93726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent)
39995	>10	H62474	Hs.108240	EST inhibitor
19328	>10	H17808	Hs.22858	ESTs
38590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
5619	>10	X14850	Hs.2711	HISTONE H2A.X
4029	>10	U21090	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15006	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
3659	>10	U04313	Hs.55279	Protease inhibitor 5 (maspin)
26916	>10	AA331393	Hs.47378	ESTs
1346	>10	HG4716-HT5158	Hs.87630	EST - HG4716-HT5158 Highly similar to CHROMOSOME CONDENSATION
37491	10.0	AA455239		PROTEIN DPY-27 [Caenorhabditis elegans]
13110	9.8	AA435840	Hs.19114	Homo sapiens mRNA for high mobility group protein HMG2a
4676	9.6	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (hGGH) mRNA complete cds
21655	8.7	R38239	Hs.25276	EST

FIG.\_2Aa

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14723	8.3	D59894 X54942	Hs.34782 Hs.83758	ESTs CDC28 protein kinase 2
5793	7.4	N22107	Hs.124215	ESTs
29848	7.1	H03686	Hs.112013	ESTs
9347	7.0	X69141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
6078	7.0	D89377	Hs.89404	Msh (Drosophila) homeo box homolog 2
9326	6.8	J05614	EST - J05614	
1566	6.7	AA129757	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
25675	6.7			
20126	6.4	N22015	Hs.18457	ESTs
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal
10867	6.1	AA088458	Hs.19322	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING
18062	6.0	AA179845	Hs.73625	ENTRY !!! [H.sapiens]
4093	5.9	U25182	Hs.83383	ESTs Moderately similar to rabkinasin-6 [M.musculus]
18290	5.8	AA211901	Hs.86430	Human antioxidant enzyme AOE37-2 mRNA complete cds
5330	5.8	U91327	EST - U91327	
4244	5.7	U33286	Hs.90073	Human chromosome segregation gene homolog CAS mRNA complete cds
6928	5.7	Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
6160	5.6	X74794	Hs.89699	CDC21 HOMOLOG
31487	5.4	N69507	Hs.129849	ESTs
9470	5.3	H46617	EST - H46617	
33458	5.0	W866835	Hs.14158	Homo sapiens mRNA for KIAA0636 protein complete cds
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds

FIG.\_2Ab

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
1106 34367	4.8 4.8	HG2981-HT3127 AA251758	Hs.40323	EST - HG2981-HT3127 Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
11595 17622	4.8 4.8	AA242819 AA131584	Hs.32539 Hs.71435	ESTs ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754 25038	4.7 4.7	AA287642 AA010065	Hs.81848 Hs.83758	Human mRNA for KIAA0078 gene complete cds CDC28 protein kinase 2
5312 8085	4.6 4.6	U90716 AA314779	Hs.79187 Hs.105484	Human cell surface protein HCAR mRNA complete cds ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
33656 8264 34479	4.6 4.5 4.5	W95477 AA401334 AA262080	Hs.50582 Hs.106941 Hs.110736	ESTs ESTs Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
7898 10716 5690 20203	4.4 4.4 4.4 4.3	AA263032 AA053319 X17620 N26855	Hs.81634 Hs.9951 Hs.118638 Hs.5858	ESTs ESTs NUCLEOSIDE DIPHOSPHATE KINASE A ESTs Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]
10923 28050 10970 4149 5767 26596 8961	4.2 4.1 4.1 4.1 4.1 4.0 3.9	AA116036 AA479139 AA129390 U28386 X53793 AA279943 AFFX-	Hs.9329 Hs.75393 Hs.5285 Hs.2397 Hs.118226 Hs.88671 AFFX-HUMTFRR/M11507_3	ESTs ESTs RAG (recombination activating gene) cohort 1 MULTIFUNCTIONAL PROTEIN ADE2 ESTs AFFX-HUMTFRR/M11507_3

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38604	3.9	AA598803	Hs.111496	ESTs MYB PROTO-ONCOGENE PROTEIN
30560	3.9	NA9284	Hs.1334	ESTs
8513	3.8	AA446990	Hs.103135	ESTs
14509	3.8	AA609943	Hs.32793	ESTs
25284	3.8	AA045074	Hs.110146	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]
27354	3.8	AA425221	Hs.81688	ESTs
18385	3.8	AA227219	Hs.110826	Homo sapiens CAGF9 mRNA partial cds
25240	3.7	AA039713	Hs.110406	ESTs
16854	3.7	AA055552	Hs.71622	ESTs Weakly similar to KIAA0319 [H.sapiens]
3709	3.7	U07550	Hs.1197	Heat shock 10 kD protein 1 (chaperonin 10)
13606	3.5	AA456437	Hs.20386	ESTs Weakly similar to CLEavage STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]
8338	3.4	AA417152	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
387	3.4	D28589	EST - D28589	
15643	3.4	W58247	Hs.27437	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
13838	3.4	AA465342	Hs.34045	ESTs
251	3.4	D14520	Hs.84728	Basic transcription element binding protein 2
3778	3.4	U09848	Hs.363	Zinc finger protein 139 (clone pHZ-37)
5660	3.4	X16396	Hs.37791	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
17365	3.4	AA101551	Hs.68900	ESTs
33985	3.3	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
19233	3.3	H12634	Hs.8104	ESTs
13767	3.3	AA463234	Hs.119387	ESTs
4738	3.3	U58766	Hs.75801	Human FX protein mRNA complete cds

**FIG.\_2Ad**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17041	3.3	AA070364 W28362 AA094800	Hs.44131 Hs.55682	EST - RC_AA070364 ESTs Human translation initiation factor eIF3 p66 subunit mRNA complete cds
15504	3.3			
7401	3.3			
18683	3.2	F04258	Hs.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE
23930	3.2	T96690	Hs.125123	[Bos taurus] ESTs Weakly similar to III ALU SUBFAMILY J WARNING
11288	3.1	AA196512 D00596	Hs.25916 Hs.82962	ENTRY !!!! [H.sapiens] ESTs Thymidylate synthase
170	3.1			
11659	3.1	AA251909 AA489080	Hs.36708 Hs.3566	Homo sapiens MAD3-like protein kinase mRNA complete cds ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]
14134	3.1			
11140	3.1	AA158132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
17925	3.0	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-R3P) mRNA complete cds
26530	3.0	AA278650 AA104023	Hs.73291 Hs.110048	ESTs
7445	3.0			
18055	3.0	AA179387 U82987	Hs.73596 Hs.87246	ESTs ESTs
15174	3.0	W93943 L24804	Hs.59509 Hs.75839	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds Human (p23) mRNA complete cds
33620	3.0			
1932	3.0			
39556	3.0	F03738 L00058	Hs.3657 Hs.79070	ESTs V-myc avian myelocytomatosis viral oncogene homolog
1605	2.9			
4536	2.9	U48705	Hs.75562	Receptor protein-tyrosine kinase EDDR1
36200	2.9	AA421164	Hs.107213	ESTs

FIG.\_2Ae

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12313	2.9	AA397916 Hs.15641 ESTs	Hs.22595	
19867	2.9	Hs.1476 X69398	Hs.15641 Hs.82685	CD47 antigen (Rh-related antigen integrin-associated signal transducer)
6081	2.9			
16708	2.8	AA043944 D26156	Hs.626663 Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
357	2.8			
8059	2.8	AA310967 AA411448 N22895	Hs.5080 Hs.139386 Hs.6831	ESTs Weakly similar to T04A8.11 [C.elegans] Homo sapiens clone 1400 unknown protein mRNA partial cds
35830	2.8			
20151	2.8	AA505133	Hs.62273	ESTs
28258	2.8	AA460077 X91788	Hs.28555 Hs.84974	ESTs H.sapiens mRNA for Ich protein
8616	2.8			
6480	2.8	AA621122	Hs.5198	ESTs
14566	2.8	AA490885	Hs.21766	ESTs
14182	2.8	AA4412528	Hs.20183	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]
35955	2.7			
17642	2.7	AA132983	Hs.44155	ESTs Moderately similar to C-1-TETRAHYDROFOLATE
6131	2.7	X72841	Hs.2758	SYNTHASE CYTOPLASMIC [H.sapiens]
				Human retinoblastoma-binding protein (RbAp46) mRNA complete cds
6444	2.7	X89750 AA215333	Hs.90077 Hs.97101	H.sapiens mRNA for TGIF protein
7701	2.7			
42534	2.7	W73189	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
34796	2.7	AA291259	Hs.97101	ESTs

FIG.\_2Af

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
1923	2.7	L23808 AA126719	Hs.1695 Hs.25282	Matrix metalloproteinase 12 (macrophage elastase) ESTs
10951	2.6	AA207114	Hs.27842	ESTs
11308	2.6	U24704	Hs.111709	Human antisecretory factor-1 mRNA complete cds
4086	2.6	X13482	Hs.80506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
5587	2.6	H59617	Hs.5199	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]
19841	2.6	AA187579 AA227261 AA476319 M64929	Hs.102696 Hs.20922 Hs.5327 Hs.75200	ESTs Weakly similar to Yel007c-ap [S.cerevisiae] ESTs ESTs Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform
7614	2.6	AA430032 X62153	Hs.7487 Hs.82479	ESTs Moderately similar to PTTG gene product [R.norvegicus] Minichromosome maintenance deficient (S. cerevisiae) 3
11362	2.6	AA497013 AA487508	Hs.142592 Hs.9877	ESTs Homo sapiens mRNA for KIAA0688 protein complete cds
13866	2.6	J02645	Hs.81613	Eukaryotic translation initiation factor 2A
2993	2.6	R43286 X92098	EST - RC_R43286 H.sapiens mRNA for transmembrane protein rnp24	
		AA285277	Hs.75914 Hs.8932	Homo sapiens brain expressed ring finger protein mRNA complete cds
		D38076 AA253031	Hs.24763 Hs.31730	RAN binding protein 1 Homo sapiens RRM RNA binding protein GRY-RBP (GRY-RBP) mRNA complete cds
452	2.4		Hs.108527	ESTs Weakly similar to No definition line found [C.elegans]
11701	2.4		Hs.19574	ESTs Highly similar to AAC-RICH mRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]
36390	2.4	AA426291		
14420	2.4	AA600322		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
6387	2.4	X85372	Hs.105465	H.sapiens mRNA for Sm protein F
1497	2.4	J04088	Hs.3378	Topoisomerase (DNA) II alpha (170kD)
27872	2.4	AA459254	Hs.48855	ESTs
8163	2.4	AA357394	Hs.98073	ESTs
23065	2.4	T23539	Hs.7165	ESTs Highly similar to zinc finger protein [M.musculus]
20837	2.4	N69263	Hs.20524	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]
17352	2.3	AA100925	Hs.20990	ESTs
28796	2.3	D51272	EST - RC_D51272_s	
26679	2.3	AA281733	Hs.4310	Homo sapiens tyrosine phosphatase PIR1 mRNA
24092	2.3	W422845	Hs.14611	complete cds
5875	2.3	X59405	Hs.83532	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)
7404	2.3	AA094989	Hs.7381	Homo sapiens voltage dependent anion channel protein mRNA complete cds
6388	2.3	X85373	Hs.77496	H.sapiens mRNA for Sm protein G
25050	2.3	AA011134	Hs.25863	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
3343	2.3	M97936	Hs.21486	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
5937	2.2	X62534	Hs.80684	High-mobility group (nonhistone chromosomal) protein 2
7387	2.2	AA093977	Hs.71475	ESTs
20843	2.2	N69352	Hs.5683	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds
28448	2.2	AA621752	Hs.76887	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds
651	2.2	D78129	EST - D78129	

**FIG.\_2Ah**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR	UNIGENE DESCRIPTOR	UNIGENE CLUSTER	ACCESSION	UPREGULATED OF TUMOR
11688	2.2	AA252672	Hs.103300	Homo sapiens diphthamide biosynthesis protein-2 (DPH2)	
11803	2.2	AA257971	Hs.21214	mRNA, complete cds	
4046	2.2	U22376	Hs.1334	ESTs	
20276	2.2	N32919	Hs.27931	MYB PROTO-ONCOGENE PROTEIN	
34370	2.1	AA251829	Hs.104058	ESTs	Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPR7 INTERGENIC REGION
14582	2.1	AA621340	Hs.10600	[Saccharomyces cerevisiae]	
3461	2.1	S75256	EST - S75256	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION	
924	2.1	HG1112-HT1112	EST - HG1112-HT1112		
24348	2.1	W86469	Tropomyosin alpha chain (skeletal muscle)		
10898	2.1	AA112063	ESTs	Weakly similar to PRE-MRNA SPLICING HELICASE	
381	2.1	D28473	BRR2 [S.cerevisiae]		
11528	2.1	AA236018	Isoleucine-tRNA synthetase		
25593	2.1	AA113149	ESTs	Weakly similar to unknown [S.cerevisiae]	
38040	2.1	AA481403	Hs.8130	Hom sapiens IPL (IPL) mRNA complete cds	
4111	2.1	U26312	Hs.107213	ESTs	
61	2.0	AC002115	Hs.83550	Human heterochromatin protein HP1Hs-gamma mRNA complete cds	
9112	2.0	D16611	Hs.83379	Cytochrome c oxidase subunit VIIb	
380	2.0	D28423	Hs.89866	Coproporphyrinogen oxidase (coproporphyrin harderoporphyrin)	
377	2.0	D28364	EST - D28423		
28379	2.0	AA609710	EST - D28364		
			Hs.42582	ESTs	

**FIG.-2Ai**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24230	2.0	W72276	Hs.5950	ESTs
40212	2.0	H88535	Hs.9564	Human clone 121711 defective mariner transposon Hsmar2
8118	2.0	AA328993	Hs.104558	mRNA sequence ESTs

*FIG.\_2Aj*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33616	>10	W93726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'5'-oligoisoadenylylate synthetase-dependent) inhibitor
39995	>10	H62474	Hs.108240	EST
19328	>10	H17808	Hs.22858	ESTs
38590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
6106	>10	X70683	Hs.83484	SRY (sex determining region Y)-box 4
8648	>10	AA465016	Hs.69423	Homo sapiens serine protease-like protease (nes1) mRNA complete cds
5619	>10	X14850	Hs.2711	HISTONE H2A.X
5603	>10	X14253	Hs.75561	Teratocarcinoma-derived growth factor 1
37677	>10	AA460530	Hs.98384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
11561	>10	AA236533	Hs.19222	Evi-1
39787	>10	H20131	Hs.107561	ESTs
16490	>10	AA026418	Hs.91539	ESTs
32240	>10	R50976	Hs.12013	Ribonuclease L (2'5'-oligoisoadenylylate synthetase-dependent) inhibitor
12480	>10	AA403116	Hs.9880	Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA complete cds

**FIG.-3Aa**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2144	>10	L41349	Hs.74014	Phospholipase C beta 4
12143	>10	AA290991	Hs.17296	ESTs
33006	>10	W46286	Hs.107039	Weakly similar to ZK1058.5 [C.elegans]
39535	>10	F02450	Hs.111980	Moderately similar to unknown protein [H.sapiens]
41005	>10	N79516	Hs.73287	ESTs
6449	>10	X89986	Hs.32936	H.sapiens mRNA for NBK apoptotic inducer protein
37653	>10	AA460017	Hs.99513	ESTs
4178	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA\ complete cds
1863	>10	L19161	Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
19787	>10	H56679	Hs.37362	ESTs
8092	>10	AA316272	Hs.24550	ESTs
37074	>10	AA446344	Hs.99068	ESTs
39405	>10	D50975	Hs.21281	ESTs
10747	>10	AA055841	Hs.31953	ESTs
5002	>10	U72761	Hs.6990	Human karyopherin beta 3 mRNA complete cds
33791	>10	Z40883	Hs.65588	ESTs
6188	>10	X76029	Hs.2841	NEUROMEDIN U-25 PRECURSOR
13136	>10	AA436560	Hs.7327	ESTs
5963	>10	X63629	Hs.2877	Cadherin 3 (P-cadherin)
38179	>10	AA487492	Hs.76272	Homc sapiens clone 23592 mRNA sequence
30938	>10	N58561	Hs.84898	Cathepsin B
34692	>10	AA285079	Hs.125873	ESTs
17987	>10	AA169379	Hs.72865	ESTs
23832	>10	T92018	Hs.16961	ESTs
36695	>10	AA433910	Hs.98786	ESTs

**FIG.-3Ab**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10233	>10	R71427	Hs.9081	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]
38330	>10	AA490882	Hs.112227	ESTs ESTs HG4747-HT5195
1349	>10	G4747-HT5195	Hs.131915	
36962	>10	AA442082	Hs.84374	Human MEK5 mRNA complete cds
4975	>10	U71088	Hs.58393	Cell division cycle 2 G1 to S and G2 to M
5510	>10	X05360	Hs.73826	Protein tyrosine phosphatase non-receptor type 4
3021	>10	MF68941	Hs.84980	ESTs
17734	>10	AA137246	Hs.109761	ESTs
36371	>10	AA426017	Hs.77770	Human mRNA for clathrin-like protein complete cds
459	>10	D38293	Hs.69588	EST
17419	>10	AA113349	Hs.34892	ESTs
14054	>10	AA485223	Hs.87465	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds
5021	>10	U73524		
4994	>10	U72514	Hs.12045	Human C2f mRNA complete cds
26355	>10	AA256379	Hs.99291	ESTs
4455	>10	U43944	Hs.14732	MALATE OXIDOREDUCTASE
10748	>10	AA055892	Hs.14543	ESTs
8111	>10	AA323787	Hs.4770	ESTs
19389	>10	H20165	Hs.31734	EST
32195	>10	R43471	Hs.22355	ESTs Weakly similar to ORF YOR258w [S.cerevisiae]
38970	>10	AA609749	Hs.112759	EST - RC_R27975
21519	>10	R27975		EST - RC_AA190888
34013	>10	AA190888		Ribonuclease L (2'5'-oligoisoadenylate synthetase-dependent)
6167	>10	X74987	Hs.12013	inhibitor

FIG.-3AC

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41107	>10	R01634	Hs.119878	ESTs
5986	>10	X64810	Hs.78977	Protein convertase subtilisin/kexin type 1
11603	>10	AA243052	Hs.16389	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]
40498	>10	N26086	Hs.132991	Homo sapiens citrate synthase mRNA complete cds
6315	>10	X81889	Hs.16381	H.sapiens mRNA for p0071 protein
4702	>10	U57341	EST - U57341	
18676	>10	F04022	Hs.27885	ESTs
24197	>10	W67277	Hs.17546	ESTs
4713	>10	U57721	Hs.81771	Human L-kynurenine hydrolase mRNA complete cds
38460	>10	AA504462	Hs.105730	ESTs
18330	>10	AA216722	Hs.54481	Human mRNA for apolipoprotein E receptor 2 complete cds
18782	>10	F09739	Hs.12562	ESTs
42766	>10	Z99394	Hs.94432	ESTs Moderately similar to !!! ALU SUBFAMILY SP WARNINGENTRY !!! [H.sapiens]
34014	>10	AA191348	Hs.96178	ESTs
16835	>10	AA054438	Hs.60753	ESTs
6384	>10	X85137	Hs.41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
29893	>10	N23003	Hs.42186	ESTs
38553	>10	AA521471	Hs.102652	ESTs
11160	>10	AA164289	Hs.26006	ESTs
1158	>10	G3344-HT3521	Hs.19736	EST - HG3344-HT3521 Weakly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME 1 [Schizosaccharomyces pombe]
7325	>10	AA090842		EST - RC_AA479294
37978	>10	AA479294	Hs.14484	ESTs Weakly similar to M01F1.4 [C.elegans]
31136	>10	N63512		

**FIG.\_3Ad**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
11813	>10	AA258158	Hs.22153	
10992	>10	AA132523	Hs.22900	Homo sapiens BAC clone RG119C02 from 7p15
5789	>10	X54925	Hs.83169	Matrix metalloproteinase 1 (interstitial collagenase)
16993	>10	AA065300	Hs.75337	Human mRNA for KIAA0035 gene partial cds
17654	>10	AA133250	Hs.62180	ESTs
20057	>10	H98079	Hs.31497	ESTs
39436	>10	D52692	Hs.74574	Human Ca2+-dependent activator protein for secretion mRNA complete cds
19727	>10	H52702	Hs.36690	ESTs
41381	>10	R42278	Hs.31748	H.sapiens mRNA for TRE5
22576	>10	R79111	Hs.29388	ESTs
35769	>10	AA406206	Hs.104746	ESTs
33980	>10	AA180223	Hs.8454	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN
40911	>10	N69114	Hs.21336	H.sapiens mRNA for orphan nuclear hormone receptor
37084	>10	AA446486	Hs.125129	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds
26935	>10	AA347193	Hs.77831	ESTs [Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]] EST - L47276
2188	>10	L47276	Hs.36820	Bloom syndrome
4362	>10	U399817	Hs.89319	ESTs
42354	>10	W19346	Hs.91447	PHOSPHATIDYLINOSITOL
9127	>10	D30037	Hs.18937	ESTs
20614	>10	N59230	Hs.2707	G1 to S phase transition 1
5692	>10	X17644	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds
4388	>10	U40714	Hs.165	Glucagon-like peptide-1 receptor
3598	>10	U01157		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24545	>10	Z38462	Hs.12403	ESTs
35309	>10	AA398660	Hs.97301	EST
23662	>10	T86674	Hs.16253	ESTs
37456	>10	AA454632	Hs.123157	ESTs
10840	>10	AA084104	Hs.30177	ESTs
25179	>10	AA031268	Hs.113319	H.sapiens mRNA for kinesin-2
21	>10	AB000905	Hs.143080	H.sapiens histone H4 gene
18762	>10	F09458	Hs.12421	ESTs
39221	>10	AA621346	Hs.99234	Homo sapiens protein phosphatase with EF-hands-1 (PPEF-1) mRNA complete cds
39232	>10	AA621409	Hs.112986	ESTs
42602	>10	W86423	Hs.105413	ESTs
22372	>10	R62831	Hs.28366	EST
39110	>10	AA620709	Hs.20563	ESTs Weakly similar to HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II [C.elegans]
16810	>10	AA053636	Hs.129849	ESTs
29645	>10	H95840	Hs.42116	ESTs
36405	>10	AA426406	Hs.10801	Homo sapiens mRNA for KIAA0530 protein partial cds
4029	>10	U21090	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15006	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
25282	>10	AA044825	Hs.103446	ESTs
34561	>10	AA280298	Hs.107119	ESTs
40594	>10	N35388	Hs.112227	ESTs
16074	>10	AA001507	Hs.59861	ESTs
27046	>10	AA400670	Hs.79507	Homo sapiens mRNA for KIAA0582 protein partial cds

FIG.-3Af

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER ACCESSION	UNIGENE DESCRIPTOR
31484	>10	N69466	Hs.49683 ESTs
39504	>10	D80632	Hs.10726 ESTs
20304	>10	N34686	Homo sapiens clone 23915 mRNA sequence
36395	>10	AA426353	ESTs
38601	>10	AA598738	Hs.98394 ESTs
40631	>10	N45124	Hs.109041 ESTs
236	>10	D13645	Hs.6809 ESTs
5623	>10	X14975	Human mRNA for KIAA0020 gene complete cds T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR
35803	>10	AA410295	Hs.139305 ESTs
5243	>10	U85946	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds
19591	>10	H40688	Hs.33785 ESTs
38828	>10	AA609177	Hs.109363 ESTs
35798	>10	AA410231	Hs.98069 ESTs
3163	>10	M84424	Hs.1355 Cathepsin E
22400	>10	R64109	Hs.28487 ESTs
20657	>10	N62889	Hs.107242 ESTs
39062	>10	AA620333	Hs.112857 EST
25082	>10	AA017257	Hs.101139 ESTs
40876	>10	N67607	p160ROCK mRNA complete cds Human Rho-associated coiled-coil containing protein kinase
5857	>10	X58377	Hs.1721 Human mRNA for adipogenesis inhibitory factor
29551	>10	H90134	ESTs
39529	>10	F02202	ESTs
6155	>10	X74331	DNA primase polypeptide 2A (58kD)
5214	>10	U83303	H.sapiens mRNA for granulocyte chemotactic protein
36958	>10	AA442060	ESTs

**FIG.-3Ag**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40660	>10	N49104	Hs.79108	NUCLEAR FACTOR RIP140
37816	>10	AA469954	Hs.104820	EST
25951	>10	AA234556	Hs.135158	EST
22072	>10	R49406	Hs.28410	ESTs
39832	>10	H26279		EST - RC_H26279
23198	>10	T40530		ESTs Weakly similar to B0035.14 [C.elegans]
29331	>10	H68116	Hs.8241	
38316	>10	AA490500	Hs.39063	ESTs
			Hs.18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20)
				mRNA complete cds
				ESTs
37829	>10	AA470084	Hs.98358	
3870	>10	U14518	Hs.1594	Centromere protein A (17kD)
39176	>10	AA621091	Hs.72087	ESTs
41793	>10	T03887	Hs.7327	ESTs
33666	>10	W95876	Hs.59741	ESTs
35766	>10	AA406169	Hs.16349	Homo sapiens KIAA0431 mRNA partial cds
32277	>10	R61493	Hs.26886	Human mRNA for rod photoreceptor protein complete cds
5558	>10	X07876	Hs.89791	Wingless-type MMTV integration site 2 human homolog
6382	>10	X85133	Hs.85273	H.sapiens RBQ-1 mRNA
41040	>10	N91948	Hs.125034	ESTs
39080	>10	AA620552		EST - RC_AA620552_r
20307	>10	N34830	Hs.37636	ESTs
18260	>10	AA206801	Hs.86277	ESTs
41065	>10	N93618	Hs.28554	ESTs
33109	>10	W59961	Hs.22564	Human mRNA for KIAA0389 gene complete cds
28015	>10	AA477421	Hs.21801	ESTs
30610	>10	N50138	Hs.47032	EST
34015	>10	AA191353	Hs.109884	ESTs

**FIG.-3Ah**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40559	>10	N33024	Hs.23450	ESTs
1445	>10	J03027	Hs.73885	MHC class I protein HLA-G
13242	>10	AA445994	Hs.21331	ESTs
37983	>10	AA479348	Hs.52871	H.sapiens mRNA for SYT
42242	>10.	T89579	Hs.79353	Homo sapiens E2F-related transcription factor (DP-1) mRNA complete cds
37135	>10	AA447540	Hs.99112	EST
20564	>10	N55443	Hs.23625	ESTs
28141	>10	AA488432	Hs.56407	ESTs
21240	>10	R08613	Hs.20188	ESTs
34382	>10	AA252512	Hs.10069	ESTs
25948	>10	AA234365	Hs.102456	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds
33953	>10	AA173290	Hs.67397	Human HOXA1 mRNA long transcript and alternatively spliced forms complete cds
40913	>10	N69218	Hs.108232	ESTs
35697	>10	AA405512	Hs.104741	ESTs
34672	>10	AA284372	Hs.111471	ESTs
3659	>10	U04313	Hs.552279	Protease inhibitor 5 (maspin)
17051	>10	AA070801	Hs.51615	ESTs
34372	>10	AA251973	Hs.143853	ESTs
19203	>10	H11593	Hs.28116	ESTs
20791	>10	N68057	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
24215	>10	W69425	Hs.15767	ESTs
37246	>10	AA449311	Hs.98658	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds

*FIG.-3Ai*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
6790	>10	Y12394	Hs.3886	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds
25806	>10	AA149007	Hs.103871	EST
1852	>10	L17328	Hs.103419	Human FEZ2 mRNA partial cds
38871	>10	AA609333	Hs.139867	EST
36307	>10	AA424803	Hs.98474	EST
25047	>10	AA011031	Hs.110182	ESTs
33343	>10	W79834	Hs.58559	ESTs Weakly similar to rhotekin [M.musculus]
5799	>10	X55330	Hs.111661	Aspartylglucosaminidase
23623	>10	T84047	Hs.15428	ESTs
13143	>10	AA436619	Hs.36353	ESTs
29523	>10	H88353	Hs.139312	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]
26291	>10	AA253422	Hs.142179	ESTs
35801	>10	AA410291	Hs.114121	ESTs
37159	>10	AA447714	EST - RC_AA447714	
40064	>10	H72283	Hs.38483	Human mRNA for KIAA0265 gene partial cds
38867	>10	AA609318	Hs.3144	Human cbl-b mRNA complete cds
29795	>10	N20641	Hs.46230	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 [Homo sapiens]
26677	>10	AA281636	Hs.888882	ESTs
5960	>10	X63575	Hs.89512	ATPase Ca++ transporting plasma membrane 2
37611	>10	AA458996	Hs.32970	(NOTE: redefinition of symbol) Human signaling lymphocytic activation molecule (SLAM)
36753	>10	AA435686	Hs.97439	mRNA complete cds
26274	>10	AA253011	Hs.88756	ESTs
32789	>10	W02779	Hs.55271	ESTs Moderately similar to kinesin-73 [D.melanogaster]

**FIG.-3Aj**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37168	>10	AA447772	Hs.125153	ESTs
39433	>10	D52037	Hs.35650	Human thymidine kinase 2 (TK2) mRNA complete cds
1570	>10	K01383	EST - K01383	
30617	>10	N50646	Hs.47083	ESTs
35106	>10	AA371561	Hs.142355	EST Weakly similar to putative p150 [H.sapiens]
30190	>10	N33264	Hs.44463	EST
789	>10	D86971	Hs.78851	Human mRNA for KIAA0217 gene partial cds
4386	>10	U40622	Hs.21523	DNA repair protein XRCC4
31944	>10	N93193	Hs.80310	ESTs
13237	>10	AA443971	Hs.142495	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
4157	>10	U28811	Hs.78979	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds
2070	>10	L37378	Hs.123074	Homo sapiens guanylyl cyclase (RetGC-2) mRNA complete cds
2123	>10	L40396	Hs.26956	Homo sapiens (clone s22i71) mRNA fragment
26926	>10	AA342402	Hs.48729	ESTs
6479	>10	X91653	EST - X91653	
11969	>10	AA280670	Hs.24968	ESTs
37601	>10	AA458864	Hs.102946	ESTs
34904	>10	AA321746	Hs.96719	EST
35958	>10	AA412550	Hs.97804	ESTs
28644	>10	D12163	Hs.103262	ESTs
38194	>10	AA487969	Hs.96692	ESTs
42177	>10	T79786	Hs.100582	ESTs
40604	>10	N38893	Hs.28578	Homo sapiens KIAA0428 mRNA complete cds
3913	>10	U16261	Hs.66576	Human MDA-7 (mda-7) mRNA complete cds

**FIG.-3AK**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23759	>10	T90313	Hs.16732	ESTs
21238	>10	R08564	Hs.51919	Plasminogen-like protein
2857	>10	M58597	Hs.2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)
34518	>10	AA278721	Hs.103104	ESTs
18008	>10	AA171895	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA sequences
19001	>10	H02890	Hs.29885	ESTs
39488	>10	D60831	Hs.126021	ESTs
23360	>10	T58531	Hs.141905	ESTs
34105	>10	AA207123	Hs.130857	ESTs
38121	>10	AA485724	EST - RC_AA485724	ESTs Moderately similar to URACIL-DNA GLYCOSYLASE
35038	>10	AA350541	Hs.106601	1 PRECURSOR [H.sapiens]
29080	>10	F13655	Hs.65638	ESTs Moderately similar to !!! ALU SUBFAMILY SB1
3196	>10	M86917	Hs.143065	WARNING ENTRY !!! [H.sapiens]
9723	>10	L4542	Hs.126923	Oxysterol binding protein
25215	>10	AA035540	Hs.1255	ESTs
2627	>10	M29610	Hs.93223	APOLIPOPROTEIN AI REGULATORY PROTEIN-1
39218	>10	AA621330	Hs.114381	Glycophorin E
20088	>10	N20054	Hs.20325	ESTs
22557	>10	R76722	Hs.29557	ESTs
30265	>10	N35115	Hs.44698	ESTs
33713	>10	Z39427	Hs.65748	ESTs
41678	>10	R80675	Hs.144133	EST
18392	>10	AA227751	Hs.55896	ESTs

FIG.-3A

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
ACCESSION			
42390	>10	W40150	Homo sapiens chromosome-associated polypeptide (HCAP) mRNA complete cds ESTs Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
38984	>10	AA609839	Hs.61060 ESTs Weakly similar to similar to t complex testis-specific protein [C.elegans]
35693	>10	AA405485	Hs.96854 ESTs MELANOMA-ASSOCIATED ANTIGEN 2 ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTR' !!! [H.sapiens]
35500	>10	AA400715	Hs.107479 ESTs Weakly similar to !!! ALU CLASS C WARNING ENTR' !!! [H.sapiens]
1856	>10	L18920	Hs.36980 ESTs Weakly similar to polypeptide
36258	>10	AA423962	Hs.108465 N-acetylgalactosaminyltransferase [H.sapiens] EST - RC_R89260 ESTs
37068	>10	AA446312	Hs.22143 ESTs EST - RC_R89260 ESTs
33020	>10	W46891	Hs.55968 ESTs EST - RC_R89260 ESTs
41719	>10	R89260	Hs.6333 ESTs
39725	>10	H11323	Hs.93753 ESTs
27037	>10	AA400198	Homo.sapiens Werner syndrome gene complete cds EST
40827	>10	N64051	Hs.48920 EST
31872	>10	N91109	Hs.54681 Human clone lota unknown protein mRNA complete cds EST
25934	>10	AA165355	Hs.80132 SQUAMOUS CELL CARCINOMA ANTIGEN 1 EST
3406	>10	S66896	Hs.37104 EST
3375	>10	S50223	Hs.108642 HKR-11 EST
37310	>10	AA451707	Hs.99246 ESTs
38235	>10	AA489030	Hs.105223 ESTs
22258	>10	R56432	Hs.26536 ESTs
787	>10	D86969	Hs.82292 Human mRNA for KIAA0215 gene complete cds ESTs
27787	>10	AA454660	Hs.44841 ESTs

*FIG.-3Am*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36845	>10	AA436198	Hs.103902	ESTs
6095	>10	X69962	Hs.89764	Fragile X mental retardation 1
28323	>10	AA599639	Hs.50216	ESTs
30207	>10	N33920	Hs.44532	H.sapiens mRNA for diubiquitin
30631	>10	N50807	Hs.47120	EST
6494	>10	X92689	Hs.55823	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
36288	>10	AA424502	Hs.98402	ESTs
37546	>10	AA456641	Hs.99433	ESTs
4193	>10	U31116	Hs.77501	Human beta-sarcoglycan A3b mRNA complete cds
25669	>10	AA128978	Hs.141982	ESTs
37777	>10	AA464860	Hs.115541	Homo sapiens Jak2 kinase mRNA complete cds
38280	>10	AA489791	EST - RC_AA489791	Eukaryotic translation initiation factor 4E
2343	>10	M15353	Hs.79306	EST - HG2036-HT2090
976	>10	G2036-HT2090		
39045	>10	AA610077	Hs.102314	ESTs
35495	>10	AA400527	Hs.111914	ESTs
3522	>10	S80267	Hs.74101	Spleen tyrosine kinase
22282	>10	R59197	Hs.21320	ESTs
32740	>10	T92950	Hs.91077	CYCL,C-AMP-DEPENDENT TRANSCRIPTION
5802	>10	X55544	Hs.36908	FACTO R ATF-1
37057	>10	AA446131	Hs.124918	ESTs
34107	>10	AA209469	Hs.96297	ESTs
34391	>10	AA252703	EST - RC_AA252703	
33301	>10	W73883	Hs.58174	ESTs
30790	>10	N52935	Hs.47580	EST

**FIG.\_3An**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38172	>10	AA487424	EST - RC_AA487424	
24915	>10	YEL003w/	EST - YEL003w/	
37492	>10	AA455248	EST - RC_AA455248	
765	>10	D86096	Prostaglandin E receptor 3 (subtype EP3) {alternative products}	
7785	>10	AA243375	EST - AA243375	
14708	>10	D59388	EST	
34070	>10	AA196549	ESTs	
6041	>10	X67155	Hs.34712	
33890	>10	HUMTFR/M11507	Hs.6592	
35277	>10	AA398536	MITOTIC KINESIN-LIKE PROTEIN-1	
26059	>10	AA236685	Hs.75530	AFFX-HUMTFR/M11507_5
25801	>10	AA148530	ESTs	
32258	>10	R55623	ESTs	
34554	>10	AA280016	Hs.97365	EST - RC_AA148530
32034	>10	N98926	Hs.58940	
4787	>10	UG1145	ESTs	
1684	>10	L07541	Hs.26434	
18718	>10	F04915	ESTs	
11121	>10	AA156359	Hs.80961	DNA polymerase gamma
38167	>10	AA487207	Hs.55209	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]
40427	>10	N21147	Hs.77256	Human enhancer of zeste homolog 2 (EZH2) mRNA
40444	>10	N22140	ESTs	complete cds
				Replication factor C (activator 1) 3 (38kD)
				ESTs
				Hs.222226
				Hs.7786
				Human TAR DNA-binding protein-43 mRNA complete cds
				EST - RC_AA487207
				Hs.121688
				ESTs
				Hs.61541
				[Euploites octocarinatus]
				ESTs
				Hs.90527
				Hs.22687
				Hs.777
				Homo sapiens platelet cG1-PDE mRNA complete cds

**FIG.\_3AO**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38211	>10	AA488687	Hs.142639	ESTs
6438	>10	X89398	Hs.78853	URACIL-DNA GLYCOSYLASE 1 PRECURSOR
38838	>10	AA609215	EST - RC_AA609215	
21412	>10	R20670	Hs.21388	ESTs
36981	>10	AA442845	Hs.98985	EST
38580	>10	AA598545	Hs.141444	ESTs
4945	>10	U69108	Hs.29736	Homo sapiens mRNA for TRAF5 complete cds
41654	>10	R76437	Hs.2001	THROMBOXANE-A SYNTHASE
41163	>10	R08176	Hs.20116	ESTs
34400	>10	AA253400	Hs.104326	ESTs
35822	>10	AA411144	Hs.104768	ESTs
40905	>10	N68738	Hs.125026	ESTs
26628	>10	AA280641	Hs.40128	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]
3799	>10	U10690	Hs.37108	Human MAGE-5a antigen (MAGE5a) gene complete cds
41752	>10	R97063	Hs.102020	ESTs
39302	>10	C14944	Hs.12136	ESTs
4680	>10	U55766	Hs.54485	Human Rev interacting protein Rip-1 mRNA complete cds
36506	>10	AA429610	Hs.98592	ESTs
40204	>10	H88296	EST - RC_H88296	
19164	>10	H10395	Hs.30980	EST
36571	>10	AA430726	EST - RC_AA430726	
26240	>10	AA252282	Hs.90438	Human mRNA for KIAA0152 gene complete cds
8963	>10	HUMTFR/M11507	Hs.128679	AFFX-HUMTFR/M11507_M
34575	>10	AA280738	ESTs	
35322	>10	AA398710	Hs.87195	H. sapiens RNA for CLCN3
1210	>10	HG37-HT37	EST - HG37-HT37	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22793	>10	R96208	Hs.35533	ESTs
36052	>10	AA417027	Hs.104787	EST
26574	>10	AA279504	Hs.88629	ESTs
31818	>10	N89774	Hs.2223	Homo sapiens mRNA for KIAA0292 gene partial cds
35197	>10	AA398120	Hs.97504	ESTs
17600	>10	AA130596	Hs.71331	ESTs
37979	>10	AA479295	Hs.106290	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]
4862	>10	U65437	Hs.95838	Human homeodomain-containing protein (HANF) mRNA complete cds
28122	>10	AA485928	Hs.69559	ESTs Weakly similar to LOK [M.musculus]
26700	>10	AA282197	Hs.89002	EST
38182	>10	AA487501	Hs.112329	ESTs
22593	>10	R79777	Hs.29897	EST
35049	>10	AA350857	Hs.22507	ESTs
40083	>10	H73466	Hs.79086	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3
7296	>10	AA085661	Hs.26023	ESTs
37615	>10	AA459101	Hs.79337	Human serine/threonine kinase mRNA partial cds
17541	>10	AA127459	Hs.108788	ESTs
19949	>10	H78263	Hs.124151	ESTs
4477	>10	U45880	Hs.37137	Human IAP-like protein ILP mRNA complete cds
26916	>10	AA331393	Hs.47378	ESTs
34188	>10	AA228030	Hs.120234	ESTs
37453	>10	AA454610	Hs.96538	ESTs
29229	>10	H48459	Hs.36232	Human mRNA for KIAA0186 gene complete cds
40760	>10	N57927	Hs.120777	ESTs Weakly similar to ELL [M.musculus]
5149	>10	U79716	Hs.12246	Human reelin (RELN) mRNA complete cds

**FIG.-3Aq**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42773	>10	L019c/MMS21		EST - YEL019c/MMS21
32189	>10	R43183	Hs.95044	ESTs
33556	>10	W90705	Hs.431	Murine leukemia viral (bmi-1) oncogene homolog
36739	>10	AA435610		EST - IRC_AA435610
31310	>10	N66831	Hs.49268	EST
26545	>10	AA278979	Hs.88547	ESTs
21902	>10	R43822	Hs.22691	EST
25925	>10	AA164494	Hs.29417	ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H.sapiens]
29344	>10	H68839	Hs.38782	EST
1346	>10	G4716-HT5158		EST - HG4716-HT5158
35874	>10	AA412024	Hs.104732	EST
218	>10	D13540	Hs.22868	PROTEIN-TYROSINE PHOSPHATASE 2C
26100	>10	AA242835	Hs.5917	Human mRNA for KIAA0391 gene complete cds
41593	>10	R64129	Hs.143745	ESTs
42290	>10	T95105	Hs.142670	ESTs
6713	>10	Y08564		EST - Y08564
6478	>10	X91648	Hs.291117	H.sapiens mRNA for pur alpha extended 3'untranslated region
33377	>10	W81219	Hs.42636	ESTs Weakly similar to F46B6.7 [C.elegans]
39329	>10	C20797	Hs.95481	EST
31619	>10	N73449	Hs.50273	ESTs
26718	10.0	AA282576	Hs.49407	ESTs
21558	10.0	R33112	Hs.100469	Human AF-6 mRNA complete cds
40113	10.0	H78003	Hs.15266	ESTs
10801	10.0	AA069285	Hs.9922	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C.elegans]

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37491	10.0	AA455239	Hs.87630	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]
23900	9.9	T95789	Hs.17669	ESTs
254	9.9	D14657	Hs.81892	Human mRNA for KIAA0101 gene complete cds
6885	9.9	Z29331	Hs.28505	Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)
29693	9.9	H97819	Hs.42453	ESTs
26482	9.9	AA262491	Hs.47222	ESTs
23123	9.9	T25306	Hs.13595	EST
26525	9.8	AA278392	Hs.43881	ESTs
13110	9.8	AA435840	Hs.19114	Homo sapiens mRNA for high mobility group protein HMGB2a
34863	9.7	AA299784	Hs.96641	Phosphoribosylglycinamide formyltransferase
39432	9.7	D51691	Hs.82285	phosphoribosylaminoimidazole synthetase
31312	9.7	N66845	Hs.136910	ESTs Weakly similar to !!! ALU CLASS B WARNING ENTR'Y !!! [H.sapiens]
21112	9.6	R01179	Hs.112536	ESTs
31572	9.6	N71294	Hs.110524	ESTs
17903	9.6	AA160259	Hs.72354	EST
20747	9.6	N66842	Hs.16395	ESTs
4676	9.6	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (hGH)
34363	9.6	AA251587	mRNA complete cds	
39094	9.5	AA620636	Homo sapiens mRNA for KIAA0530 protein partial cds	
3888	9.5	U15128	Hs.112264	ESTs
			Hs.36573	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39386	9.5	D12184 AA203742	Hs.3350 Hs.38057	ESTs ESTs
7674	9.4	U31099	Hs.121479	Human DP prostanoid receptor (PTGDR) mRNA partial cds
4192	9.4	U47050	Hs.24852	Human putative calcium influx channel (htrp3) mRNA complete cds
4507	9.4			
35606	9.4	AA402227	Hs.97345	ESTs Moderately similar to N-tropomodulin [R.norvegicus]
4970	9.4	U70862 H58813	Hs.23442 Hs.37629	Human nuclear factor I-B2 (NFIB2) mRNA complete cds
19829	9.3	T40145	Hs.21921	EST
14837	9.3	AA099585	Hs.41175	ESTs
17336	9.3	N30160	Hs.101459	ESTs
40541	9.3	H85434	Hs.40672	EST
29496	9.2	N24786	Hs.42993	ESTs Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
29943	9.2			
17997	9.2	AA169633 R11673	Hs.72835 Hs.18957	EST ESTs
21320	9.1	AA476917	Hs.34627	ESTs Weakly similar to No definition line found [C.elegans]
13883	9.1	N49072	Hs.93968	ESTs
30539	9.1	W02063	Hs.55231	EST
32778	9.1	AA257012	Hs.88054	EST
26380	9.1	X95632	Hs.86870	Human Abl interactor 2 (Abi-2) mRNA complete cds
15888	9.1	N63419	Hs.83389	ESTs
40812	9.0	D90070	Hs.96	ATL-derived PMA-responsive (APR) peptide
903	9.0	R87160	Hs.33665	ESTs
22674	9.0	N62995	Hs.58593	TRANSCRIPTION INITIATION FACTOR IIF BETA SUBUNIT
40807	9.0	W00904	Hs.8037	ESTs
15244	8.9	R67075	Hs.2074	Zinc finger protein X-linked
32296	8.9			

**FIG. 3A**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18269	8.9	AA209467	Hs.92489	ESTs
19662	8.9	H47391	Hs.33947	ESTs
41607	8.8	R67868	Hs.82767	CLEAVAGE SIGNAL-1 PROTEIN
2548	8.8	M25897	Hs.81564	Platelet factor 4
7736	8.8	AA232121	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds
34490	8.8	AA262354	Hs.111395	ESTs
38658	8.8	AA599477	Hs.103345	ESTs
7528	8.8	AA149543	Hs.5316	ESTs
39939	8.8	H53454	EST - FC_H53454	
25111	8.7	AA020787	Hs.110291	ESTs
21655	8.7	R38239	Hs.25276	EST
39663	8.7	H04756	Hs.109646	ESTs Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT [Bos taurus]
1042	8.7	G2510-HT2606	EST - HG2510-HT2606	
32330	8.6	R77776	Hs.18103	ESTs
25382	8.6	AA059007	Hs.61126	ESTs
27074	8.6	AA401475	Hs.39733	ESTs Weakly similar to C36B1.3 [C.elegans]
3955	8.5	U18259	Hs.3076	MHC class II transactivator
4959	8.5	U70322	Hs.82925	Human transportin (TRN) mRNA complete cds
2315	8.5	M14123	EST - M14123_xpt1	
37253	8.5	AA449357	Hs.17731	ESTs
39624	8.5	F10836	Hs.101234	ESTs
23213	8.5	T40891	Hs.8330	ESTs
2798	8.5	M54995	Hs.2164	Connexine tissue activation peptide III
41154	8.4	R07499	Hs.141384	ESTs
32479	8.4	T16282	Hs.75188	WEE1-LIKE PROTEIN KINASE
41251	8.4	R28279	Hs.71848	Human clone 23548 mRNA sequence

**FIG.-3Au**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19081	8.4	H06701	Hs.27948	ESTs Weakly similar to RHOMBOTIN-1 [H.sapiens]
21098	8.3	R00545	Hs.18930	ESTs
14723	8.3	D59894	Hs.34782	ESTs
37154	8.3	AA447666	Hs.77204	Human CENP-F kinetochore protein mRNA complete cds
8068	8.3	AA313387	Hs.133101	ESTs Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK10913.1 IN CHROMOSOME III [Caenorhabditis elegans]
7485	8.3	AA129547	Hs.81688	ESTs
16501	8.3	AA026969	Hs.61423	ESTs
34527	8.2	AA279091	Hs.104420	ESTs
6700	8.2	Y07867	Hs.38842	H.sapiens mRNA for Piiriin isolate 1
2852	8.2	M58460	Hs.91728	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds
11188	8.2	AA172372	Hs.20608	ESTs
42293	8.2	T95333	Hs.1222730	ESTs Weakly similar to coded for by C. elegans cDNA yk110g8.3 [C.elegans]
5443	8.2	X02530	Hs.2248	Interferon (gamma)-induced cell line protein 10 from
40937	8.2	N70607	Hs.142460	ESTs
23371	8.1	T59505	EST - RG_T59505	
26272	8.1	AA252981	Hs.87699	ESTs Weakly similar to K07C11.10 gene product [C.elegans]
17306	8.1	AA086201	Hs.92702	ESTs
18497	8.1	AA2333795	Hs.65828	ESTs
235	8.1	D13644	Hs.140933	Human mRNA for KIAA0019 gene complete cds
24525	8.1	Z38347	Hs.118338	ESTs
7826	8.1	AA248884	EST - AA248884	
32142	8.1	R38715	Hs.123918	Homo sapiens clone 24540 mRNA sequence
39067	8.1	AA620405	Hs.112860	ESTs
6235	8.0	X78416	Hs.3155	Casein alpha S1
29517	8.0	H88261	Hs.41116	ESTs

**FIG.-3Av**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28570	8.0	C21104	Hs.110776	Homo sapiens STAT-induced STAT inhibitor-2 mRNA complete cds
39344	7.9	C21034	Hs.76822	ESTs   moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]
18951	7.9	H00580	Hs.29889	ESTs
18953	7.9	H00615	Hs.24227	ESTs
18376	7.9	AA226925	Hs.88057	ESTs
19830	7.8	H58911	Hs.26645	ESTs
36023	7.8	AA416881	Hs.97383	ESTs
13347	7.8	AA449238	Hs.26838	ESTs
36614	7.8	AA431466	Hs.107319	ESTs
2192	7.8	L48211	Hs.20954	Homo Sapiens angiotensin II receptor gene complete cds
33016	7.8	W46577	Hs.41716	H.sapiens mRNA for ESM-1 protein
17215	7.8	AA083044	Hs.144225	ESTs
34894	7.8	AA311881	Hs.96700	EST
40614	7.7	N39257	Hs.99291	ESTs
36295	7.7	AA424534	Hs.98415	ESTs
19564	7.7	H38833	Hs.32838	ESTs
16914	7.7	AA058665	Hs.23744	ESTs
35967	7.6	AA412694	Hs.6891	Human splicing factor SRp55-2 (SRp55) mRNA complete cds
21672	7.6	R38635	Hs.12328	ESTs
19918	7.6	H69787	Hs.14699	ESTs
10511	7.6	AA024482	Hs.9029	ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 [Homo sapiens]
17721	7.6	AA136590	Hs.71711	ESTs
42302	7.6	T96130	Hs.137551	EST
26134	7.6	AA243763	Hs.87694	ESTs

**FIG.-3Aw**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18766	7.6	F09497	Hs.12755	
34492	7.5	AA262439	Hs.96	ATL-derived PMA-responsive (APR) peptide
270	7.5	D14822		EST - D14822
35975	7.4	AA412738	Hs.3688	ESTs
29842	7.4	N21688	Hs.43050	ESTs
35389	7.4	AA399955	Hs.97558	ESTs
19979	7.4	H88477	Hs.124237	ESTs
5793	7.4	X54942	Hs.83758	CDC2E; protein kinase 2
19978	7.4	H87770		EST - RC_H87770
1280	7.4	G4126-HT4396		EST - HG4126-HT4396
31571	7.4	N71250	Hs.50004	ESTs
23765	7.4	T90443	Hs.15053	ESTs Weakly similar to KIAA0376 [H.sapiens]
35123	7.3	AA380927	Hs.97113	EST
38252	7.3	AA489247	Hs.105234	ESTs
38216	7.3	AA488861	Hs.134943	ESTs
29418	7.2	H77915		EST - RC_H77915
4834	7.2	U63541	Hs.20225	Human mRNA expressed in HCHCC livers and Molt-4 proliferating cells partial sequence
42504	7.2	W69803	Hs.103159	ESTs
61111	7.2	X71125	Hs.79033	H.sapiens mRNA for glutamine cyclotransferase
41773	7.2	T03024	Hs.29170	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]
9951	7.1	N71513	Hs.39328	ESTs
28109	7.1	AA485212	Hs.9591	ESTs
988	7.1	G2160-HT2230		EST - HG2160-HT2230
29848	7.1	N22107	Hs.124215	ESTs
30628	7.1	N50744	Hs.124025	ESTs
22567	7.0	R77771	Hs.129445	ESTs

**FIG.-3Ax**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9347	7.0	H03686	Hs.112013	ESTs
11696	7.0	AA252894.	Hs.20474	ESTs
40584	7.0	N34870	Hs.102520	EST
193	7.0	D10923	Hs.137555	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74
18305	7.0	AA214048	Hs.259	Collagen type IV alpha 4
6078	7.0	X69141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
26741	6.9	AA283198	Hs.89113	ESTs
35069	6.9	AA358397	Hs.97007	EST
23504	6.9	T71042	Hs.12066	ESTs
299	6.9	D16815	Hs.37288	Homo sapiens orphan nuclear hormone receptor BD73 mRNA 3' end
40583	6.9	N34855	Hs.109099	ESTs
31428	6.9	N68594	Hs.125029	ESTs
6169	6.9	X75091	Hs.75055	SET PROTEIN
39524	6.9	F01905	Hs.14732	MALATE OXIDOREDUCTASE
34578	6.8	AA280837	Hs.111429	ESTs
38678	6.8	AA599920	Hs.141503	Small inducible cytokine A5 (PRNTES)
23936	6.8	T96930	Hs.15553	ESTs
9326	6.8	D89377	Hs.89404	Msh (Drosophila) homeo box homolog 2
19188	6.8	H11255	Hs.12887	ESTs Highly similar to ACTIN-LIKE PROTEIN [Bos taurus]
18185	6.8	AA194983	Hs.81791	Homo sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds
27028	6.8	AA399630	Hs.94396	ESTs Weakly similar to KIAA0371 [H.sapiens]
41289	6.8	R37265	Hs.106266	EST
34511	6.7	AA278298	EST - IRC_AA278298	
1566	6.7	J05614	EST - J05614	

FIG. 3AY

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25675	6.7	AA129757	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
5814	6.7	X56088	Hs.1644	CYTOCHROME P450 VII
13861	6.6	AA470145	Hs.25130	ESTs
29794	6.6	N20598	Hs.94288	ESTs
39333	6.6	C20910	Hs.23960	Cyclin 31
3770	6.6	U09609	Hs.73090	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
31831	6.6	N89894	Hs.91454	ESTs
33063	6.6	W53000	Hs.56155	Homo sapiens clone 24431 mRNA sequence
20326	6.6	N35583	Hs.8768	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]
34384	6.6	AA252537	Hs.96499	ESTs
25599	6.5	AA114091	Hs.44898	Human (clone 8B1) Br-cadherin mRNA complete cds
39749	6.5	H14988	Hs.107375	ESTs
42596	6.5	W85900	Hs.109333	ESTs
39606	6.5	F10243	Hs.140873	ESTs Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]
14617	6.5	C14983	Hs.37380	ESTs
27831	6.5	AA456044	Hs.40367	ESTs
34896	6.4	AA312551	Hs.96703	EST
27360	6.4	AA425356	Hs.89306	ESTs
20126	6.4	N22015	Hs.18457	ESTs
6663	6.4	Y00291	Hs.82783	RETINOIC ACID RECEPTOR BETA-2
30692	6.4	N51563	Hs.47044	ESTs
36472	6.4	AA428633	Hs.98604	EST
9578	6.4	H87652	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds

**FIG.-3Az**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR	
				UNIGENE	
39670	6.4	H05626	Hs.6921	ESTs	
22697	6.4	R89218	Hs.34256	ESTs	
37308	6.4	AA451694	Hs.99244	EST	
16101	6.4	AA002147	Hs.59952	EST	
20629	6.3	N59798	Hs.18917	ESTs	
36100	6.3	AA417740	Hs.96345	ESTs	
15488	6.3	W28097	Hs.101664	Homo sapiens clone 23711 unknown mRNA partial cds	
36667	6.3	AA432136	Hs.98682	ESTs	
30766	6.3	N52627		EST - FIC_N52627	
32882	6.3	W37683	Hs.55080	ESTs	
18072	6.3	AA180448	Hs.144300	EST	
18231	6.3	AA199747	Hs.79025	Human mRNA for KIAA0096 gene partial cds	
38282	6.3	AA489814	Hs.105299	EST	
28125	6.3	AA486073	Hs.57362	ESTs	
37464	6.2	AA454747	Hs.14934	ESTs	
36618	6.2	AA431478	Hs.98739	ESTs	
5082	6.2	U78524	Hs.75251	Human Gu binding protein mRNA partial cds	
1441	6.2	J02963	Hs.785	Integrin alpha 2b (platelet glycoprotein IIb of IIIa complex antigen CD41B)	
42105	6.1	T67710	Hs.105780	ESTs	
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal	
32570	6.1	T30222	Hs.4220	ESTs Weakly similar to tetracycline transporter-like protein [M.musculus]	
32504	6.1	T17063	Hs.65721	EST	
23335	6.1	T56804	Hs.10104	EST	
10867	6.1	AA088458	Hs.19322	ESTs Weakly similar to ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30883	6.1	N56923	Hs.48000	EST
14528	6.1	AA620295	Hs.99821	ESTs
29454	6.1	H81308	Hs.40253	EST
6798	6.1	Y13153	Hs.28526	Hom <sub>U</sub> sapiens mRNA for kynureine 3-monooxygenase
21248	6.1	R08871	Hs.14880	ESTs
21940	6.0	R44538	Hs.140889	ESTs
29066	6.0	F10927	Hs.66163	Hom <sub>U</sub> sapiens clone 23636 mRNA sequence
18774	6.0	F09609	Hs.12867	ESTs
36722	6.0	AA435512	Hs.96856	ESTs
18062	6.0	AA179845	Hs.73625	ESTs Moderately similar to rabkinasin-6 [M. musculus]
22989	6.0	T16305	Hs.49349	ESTs
41745	6.0	R95895	Hs.142677	ESTs
8787	6.0	AA504307	Hs.96264	X-LINKED HELICASE II
20550	6.0	N55013	Hs.35100	ESTs
26470	5.9	AA262179	Hs.108470	ESTs
16574	5.9	AA031926	Hs.138960	EST
693	5.9	D80007	Hs.45028	Human mRNA for KIAA0185 gene partial cds
4093	5.9	U25182	Hs.83383	Human antioxidant enzyme AOE37-2 mRNA complete cds
1192	5.9	G3546-HT3744	EST .. HG3546-HT3744	
22956	5.9	T10248	Hs.4280	ESTs
36723	5.9	AA435524	Hs.97483	EST
2114	5.9	L40384	EST .. L40384	
26872	5.9	AA291137	Hs.109270	ESTs
6602	5.9	X98266	EST .. X98266_cds2	
42701	5.9	Z38612	Hs.144000	ESTs
28573	5.8	C21118	Hs.84541	ESTs
18290	5.8	AA211901	Hs.86430	ESTs

**FIG.-3Bb**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
732	5.8	D83781	Hs.22559	Hurn an mRNA for KIAA0197 gene partial cds
5330	5.8	U91327	EST - U91327	
33503	5.8	W88720	Hs.59196	EST
2553	5.8	M26167	Hs.72933	Hurman platelet factor 4 variation 1 (PF4var1) gene complete cds
34705	5.8	AA286907	Hs.99692	EST; Weakly similar to putative p150 [H.sapiens]
42665	5.8	W93659	Hs.106932	EST; EST - RC_AA487495
38180	5.8	AA487495		
4244	5.7	U33286	Hs.90073	Human chromosome segregation gene homolog CAS mRNA complete cds
32822	5.7	W16834	Hs.55378	EST; Retinal pigment epithelium-specific protein (65kD)
3977	5.7	U18991	Hs.2133	
24673	5.7	Z39301	Hs.7859	EST; SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
6928	5.7	Z46629	Hs.2316	
38726	5.7	AA608733	Hs.138663	EST; Human mRNA for KIAA0029 gene partial cds
39290	5.7	C14573	Hs.75383	
11405	5.7	AA232231	Hs.24596	EST; Homo sapiens meltin-L precursor (ADAM12) mRNA complete cds
22538	5.7	R73567	Hs.8850	
40747	5.7	N56872	Hs.11175	Homo sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds
31596	5.7	N72094	Hs.43234	EST; EST - X82279
6329	5.6	X82279		
31578	5.6	N71361	Hs.50019	
33207	5.6	W70051	Hs.86178	H.sapiens mRNA for M-phase phosphoprotein mpp9
2545	5.6	M25753	Hs.23960	Cyclin B1

**F/G.-3BC**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22580	5.6	R79156	Hs.29613	ESTs
33592	5.6	W93127	Hs.59422	ESTs
28843	5.6	D60252	Hs.113619	ESTs
6160	5.6	X74794	Hs.89699	CDC21 HOMOLOG
37987	5.6	AA479666	Hs.105576	ESTs
42515	5.5	W72116	Hs.106333	Homo sapiens clone 23622 mRNA sequence
4732	5.5	U58522	Hs.84713	Human huntingtin interacting protein (HIP2) mRNA complete cds
3299	5.5	M95623	Hs.82609	Hydroxymethylbilane synthase
28320	5.5	AA599574	Hs.65370	ESTs
746	5.5	D84454	Hs.21899	Human mRNA for UDP-galactose translocator complete cds
39373	5.5	C21517	Hs.83313	ESTs
3117	5.4	M81182	Hs.76781	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)
21257	5.4	R09196	Hs.20321	ESTs; Moderately similar to M-phase phosphoprotein 11 [H.sapiens]
31487	5.4	N69507	Hs.129849	ESTs
28954	5.4	F03153	Hs.90383	ESTs
38928	5.4	AA609595	Hs.109960	ESTs
29903	5.4	N23366	Hs.93664	EST
30925	5.3	N58295	Hs.144393	ESTs; Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]
19091	5.3	H07864	Hs.21734	ESTs
28209	5.3	AA491250	Hs.54990	ESTs
9470	5.3	H46617	EST - H46617	
9435	5.3	H30201	EST - H30201	
28552	5.3	C20914	Hs.84497	ESTs
27411	5.3	AA428137	Hs.86434	ESTs

**FIG.-3Bd**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30615	5.3	N50556	Hs.47076	ESTs
28313	5.3	AA599309	Hs.60886	ESTs
39321	5.3	C20632	Hs.7972	ESTs
29934	5.3	N24194	Hs.43531	ESTs
1094	5.2	G2846-HT2983	EST · HG2846-HT2983	
39578	5.2	F08925	Hs.48610	ESTs
11232	5.2	AA186804	Hs.25740	ESTs Weakly similar to unknown [S.cerevisiae]
2466	5.2	M21539	Hs.2421	Human small proline rich protein (spril) mRNA clone 1292
26843	5.2	AA287450	Hs.93842	ESTs
40331	5.2	H97562	Hs.4206	ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 [Sepia officinalis]
8035	5.2	AA305116	EST · AA305116	
29793	5.2	N20593	Hs.128781	ESTs Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]
34109	5.1	AA210722	Hs.104158	EST
26408	5.1	AA258177	Hs.38399	ESTs Weakly similar to ROSA26AS [M.musculus]
19263	5.1	H15054	Hs.22184	ESTs
24596	5.1	Z38810	Hs.27194	ESTs
28589	5.1	C21245	Hs.11171	H.sapiens mRNA for apoptosis specific protein
5684	5.1	X17098	Hs.108938	Pregnancy-specific beta-1 glycoprotein 6
30710	5.1	N51761	Hs.47338	EST
35765	5.1	AA406167	Hs.98028	EST
26360	5.1	AA256460	Hs.44610	ESTs
2351	5.1	M15796	Hs.78996	Proliferating cell nuclear antigen
30262	5.1	N35065	Hs.44690	Hom sapiens clone 24739 mRNA sequence
41792	5.1	T03886	Hs.100265	ESTs
36710	5.1	AA434411	Hs.98806	ESTs

**F/G.\_3Be**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39090	5.1	AA620628	Hs.112358	ESTs
42185	5.1	T79951	Hs.111805	ESTs
18745	5.0	F09134	Hs.12839	ESTs
35746	5.0	AA406063	Hs.98003	ESTs
35356	5.0	AA399053	Hs.97529	EST
36769	5.0	AA435750	Hs.98830	EST
36900	5.0	AA436866	Hs.86178	H.sapiens mRNA for M-phase phosphoprotein mpp9
27595	5.0	AA443328	Hs.12544	ESTs
16290	5.0	AA016145	Hs.42979	ESTs
27117	5.0	AA405098	Hs.38178	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]
4304	5.0	U36764	Hs.89996	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit
33458	5.0	W86835	Hs.14158	Homo sapiens mRNA for KIAA0636 protein complete cds
26693	5.0	AA282120	Hs.88975	EST
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
29701	5.0	H97970	Hs.42476	EST
20480	5.0	N52168	Hs.22970	ESTs
8720	4.9	AA481218		EST .. AA481218
34828	4.9	AA292436	Hs.27621	Homo sapiens semaphorin F homolog mRNA complete cds
14985	4.9	U15128	Hs.36573	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
16115	4.9	AA004420	Hs.49360	ESTs
42506	4.9	W70074	Hs.103163	EST
34761	4.9	AA287833	Hs.99668	ESTs
11870	4.9	AA262587	Hs.20137	ESTs
23211	4.9	T40889	Hs.8329	ESTs

**FIG.\_3Bf**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40611	4.9	N39138	Hs.106794	Homo sapiens mRNA for KIAA0584 protein partial cds
42611	4.9	W87006	Hs.79440	Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete cds
39652	4.9	H03099	Hs.101619	ESTs
17581	4.9	AA129395	Hs.71139	EST
37239	4.9	AA449121	Hs.99210	ESTs
18712	4.9	F04677	Hs.12381	ESTs
30709	4.9	N51752	Hs.47334	ESTs 'Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]' ESTs   highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]
34179	4.9	AA227903	Hs.41127	
21433	4.8	R22183	Hs.144123	EST
39731	4.8	H11760	Hs.23606	ESTs
31295	4.8	N66653	Hs.94181	ESTs
24647	4.8	Z39108	Hs.27285	EST
31292	4.8	N66615	Hs.49232	ESTs
1285	4.8	G4157-HT4427	EST - HG4157-HT4427	
1106	4.8	G2981-HT3127	EST - HG2981-HT3127	
18212	4.8	AA196506	Hs.86076	
34367	4.8	AA251758	Hs.40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA, complete cds
34802	4.8	AA291468	Hs.98504	ESTs
34762	4.8	AA287834	Hs.109909	ESTs
11595	4.8	AA242819	Hs.32539	ESTs
8295	4.8	AA405082	Hs.125014	ESTs
17622	4.8	AA131584	Hs.71435	ESTs 'Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]'  <b>FIG.-3Bg</b>

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
35781	4.8	AA406335 AA287642	Hs.95187 Hs.81848	ESTs Human mRNA for KIAA0078 gene complete.cds
34754	4.7	T47291	Hs.8610	EST
23237	4.7	AA460318	Hs.110165	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]
37667	4.7			
11568	4.7	AA236786 AA598967	Hs.26076 Hs.141982	ESTs ESTs
38622	4.7	U79296	Hs.74642	Dihydroipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
5137	4.7			CD/C28 protein kinase 2
25038	4.7	AA010065 H16567	Hs.83758 Hs.21253	ESTs Collagen type I alpha-2
19288	4.7	T17045	Hs.90283	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT
32503	4.7	M94055	Hs.54499	Integral transmembrane protein 1
3278	4.7	L38961	Hs.89650	Homo sapiens putative DNA methyltransferase (DNMT2)
9696	4.7	AA399591	Hs.97681	mRNA complete cds
35400	4.7			EST Weakly similar to HSP60 protein [M.musculus]
35246	4.7	AA398367 AA426270	Hs.97617 Hs.98498	ESTs ESTs
36387	4.7	R27314	Hs.23820	ESTs
21509	4.7	N67889	Hs.49397	ESTs
31381	4.7	AA282781	Hs.95321	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]
26723	4.7			Human GAP SH3 binding protein mRNA complete cds
36326	4.7	AA425151	Hs.79310	EST - RC_AA113136
17409	4.7	AA113136	Hs.84149	Human mitogen-activated kinase kinase 5 (MAPKK5)
4908	4.7	U67156		mRNA complete cds
30594	4.6	N49967	Hs.46624	ESTs

**FIG.-3Bh**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38286	4.6	AA489847	Hs.112019	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang].
13073 40435	4.6 4.6	AA433950 N21614	Hs.22530 Hs.100358	ESTs Homo sapiens basic-leucine zipper transcription factor MafG (MAFG) mRNA complete cds
14474	4.6	AA609427	Hs.24164	ESTs Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]
38213 5312	4.6 4.6	AA488847 U90716	Hs.111380 Hs.79187	ESTs Weakly similar to putative p150 [H.sapiens] Human cell surface protein HCAR mRNA complete cds
24225	4.6	W70326	Hs.16506	ESTs
35588	4.6	AA401750	Hs.97343	EST
29739	4.6	H99626	Hs.42710	EST
7203	4.6	AA053096 L41939	EST - AA053096 Hs.89403	EST - AA053096 Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA :complete cds
2157	4.6	R11510	Hs.52054	ESTs
32086 8085	4.6 4.6	AA314779	Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
224	4.6	D13633	Hs.77695	Human mRNA for KIAA0008 gene complete cds
34006	4.6	AA188761	Hs.80961	DNA polymerase gamma
33656	4.6	W95477	Hs.50582	ESTs
34065	4.6	AA195517	Hs.111160	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
6028	4.5	X66503	Hs.90011	Adenylosuccinate synthase
4166	4.5	U29463	Hs.108102	Cytochrome B561
40262	4.5	H93562	Hs.100624	ESTs
22687	4.5	R88209	Hs.34161	ESTs

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41069	4.5	N93969	Hs.91107	H.sapiens mRNA for hFat protein
8264	4.5	AA401334	Hs.106941	ESTs
27588	4.5	AA443187	Hs.41181	ESTs
35882	4.5	AA412047	Hs.122578	ESTs
34479	4.5	AA262080	Hs.110736	Hum <u>en</u> bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
15921	4.5	Y12065	Hs.5092	Homo sapiens mRNA for nucleolar protein hnOp56
11279	4.4	AA195399	Hs.24641	ESTs
39222	4.4	AA621348	Hs.110042	ESTs Highly similar to DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]
34428	4.4	AA256526	Hs.121002	ESTs
8771	4.4	AA491188	Hs.62273	ESTs
22193	4.4	R53891	Hs.108805	Homo sapiens mRNA from chromosome 5q21-22 clone:A3-A
7898	4.4	AA263032	Hs.81634	ESTs
19902	4.4	H66736	Hs.34180	ESTs
9276	4.4	D82374	Hs.131854	ESTs
10716	4.4	AA053319	Hs.9951	ESTs
13193	4.4	AA442763	Hs.20483	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]
5690	4.4	X17620	Hs.118638	NUC1.EOSIDE DIPHOSPHATE KINASE A
35102	4.4	AA371509	EST · RC_AA371509	
17983	4.4	AA169226	Hs.72782	ESTs
24962	4.3	HUMTFRR/M11507	AFFX-HUMTFRR/M11507_5	
31680	4.3	N74438	Hs.50492	ESTs
27168	4.3	AA410258	Hs.85908	ESTs
28731	4.3	D20981	Hs.92453	EST

**FIG.-3Bj**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28348	4.3	AA608752	Hs.71969	ESTs
16335	4.3	AA018587	Hs.40515	ESTs Weakly similar to !!!! ALU-SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]
33036	4.3	W48580	Hs.39972	ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]
30180	4.3	N33144	Hs.44441	ESTs, Weakly similar to !!! ALU SUBFAMILY SQ WARNING
35591	4.3	AA401758	Hs.78041	ESTs, Weakly similar to !!! ALU SUBFAMILY SQ WARNING !!! [H.sapiens]
25340	4.3	AA054554	Hs.95313	EST
28106	4.3	AA485084	Hs.110462	ESTs
38690	4.3	AA600121	Hs.111467	ESTs
20203	4.3	N26855	Hs.5858	ESTs, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]
10251	4.3	R76185	Hs.18171	ESTs, Weakly similar to C01H6.7 [C.elegans]
12684	4.3	AA417558	Hs.25206	ESTs
31636	4.3	N73680	Hs.57435	Natural resistance-associated macrophage protein 2
20769	4.2	N67277	Hs.9403	ESTs
1572	4.2	K01884	EST - K01884	
10923	4.2	AA116036	Hs.9329	ESTs
34380	4.2	AA252414	Hs.104300	ESTs
10132	4.2	R35733	EST - R35733	
16629	4.2	AA036811	Hs.61859	ESTs
25146	4.2	AA026356	Hs.108106	ESTs
28730	4.2	D20959	Hs.5858	ESTs, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]
10200	4.2	R64521	Hs.77361	ESTs
38695	4.2	AA600176	Hs.112345	ESTs

**FIG.-3Bk**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
31365	4.2	N67550 WV37999	Hs.48907 Hs.103018	ESTs ESTs
42379	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
28050	4.1	M29474	Hs.73958	Human recombination activating protein (RAG-1) gene
2620	4.1			complete cds
8927	4.1	AF008442	Hs.5409	Human sapiens RNA polymerase I subunit hRPA39 mRNA
				complete cds
13379	4.1	AA449741 U79293	Hs.4029 Hs.90802	ESTs Weakly similar to AF-9 PROTEIN [H.sapiens] Human clone 23948 mRNA sequence
5134	4.1	M29581	Hs.2077	Zinc finger protein 8 (clone HF.18)
2626	4.1	AA4479969	Hs.105624	ESTs
38005	4.1	AA4431085	Hs.98706	EST
36575	4.1	AA213620	Hs.48301	ESTs Weakly similar to putative p150 [H.sapiens]
18296	4.1	H88953	EST · RC_H88953	EST · RC_H88953
29531	4.1	HUMTFR/M11507	AFFX-HUMTFR/M11507_5	
143	4.1	AA129390	Hs.5285	
10970	4.1	AA152305	Hs.2248	Interferon (gamma)-induced cell line protein 10 from
25836	4.1	H53038	Hs.36710	EST
19735	4.1	N53564	Hs.108159	ESTs
40711	4.1	U28386	Hs.2397	RAG (recombination activating gene) cohort 1
4149	4.1	X53793	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
5767	4.1	X05232	Hs.83326	Stromelysin
5503	4.1	N34893	Hs.6153	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN
20310	4.1	D38145 AA248406 H90161	B028.9 IN CHROMOSOME III [Caenorhabditis elegans]	B028.9 IN CHROMOSOME III [Caenorhabditis elegans]
456	4.1		Hs.61333	Prostaglandin I2 (prostacyclin) synthase
7814	4.1		Hs.19347	ESTs
40230	4.0		Hs.64592	ESTs

**FIG.-3B1**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR	
				ESTs	
33651	4.0	W95409	Hs.59704	ESTs	
16777	4.0	AA046968	Hs.62823	EST	
19110	4.0	H08778	Hs.133521	ESTs	
34442	4.0	AA258093	Hs.108642	HKR-T1	
5099	4.0	U79247	Hs.90796	Human clone 23599 mRNA sequence	
8209	4.0	AA384220	Hs.86605	ESTs	
24408	4.0	W90146	Hs.35962	ESTs	
26596	4.0	AA279943	Hs.88671	ESTs	
16485	4.0	AA026269	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncoyene spi1	
32969	4.0	W42451	Hs.92260	ESTs	
27006	4.0	AA398695	Hs.56159	ESTs Weakly similar to E04F6.2 gene product [C. elegans]	
29809	4.0	N21043	Hs.42932	EST	
9596	3.9	H91564	Hs.13540	ESTs	
29024	3.9	F09315	Hs.76982	Homo sapiens mRNA for KIAA0583 protein partial cds	
21694	3.9	R39317	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	
13207	3.9	AA443321	Hs.101810	ESTs	
37865	3.9	AA476623	Hs.99819	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL- TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]	
36201	3.9	AA421164	Hs.107213	ESTs	
8961	3.9	HUMTFR/M11507	AFFY-HUMTFR/M11507_3		
17444	3.9	AA115933	Hs.42323	ESTs	
25869	3.9	AA157267	Hs.144332	ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24862	3.9	Z41415	Hs.6823	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
26685	3.9	AA281950	Hs.79656	ESTs
42300	3.9	T95850	Hs.100703	ESTs
6495	3.9	X92715	Hs.3057	Zinc finger protein 74 (Coss52)
38604	3.9	AA598803	Hs.111496	ESTs
36358	3.9	AA425756	Hs.98445	ESTs
30560	3.9	N49284	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
14413	3.9	AA600150	Hs.14366	ESTs
23823	3.9	T91805	Hs.38084	Homo sapiens mRNA for ST1C2 complete cds
38158	3.9	AA487021	Hs.105703	EST
2572	3.9	M27281	Hs.73793	Vascular endothelial growth factor
40100	3.8	H75933	Hs.75901	Lamin.n receptor (2H5 epitope)
40258	3.8	H93340	Hs.125010	ESTs
20944	3.8	N74443	Hs.16247	ESTs
20411	3.8	N48963	Hs.21992	Homo sapiens mRNA for KIAA0689 protein partial cds
10345	3.8	AA001663	Hs.7959	ESTs
31261	3.8	N66248	Hs.141609	EST
8513	3.8	AA446990	Hs.103135	ESTs
13877	3.8	AA476604	Hs.7114	ESTs
40748	3.8	N56879	Hs.102633	EST
14509	3.8	AA609943	Hs.32793	ESTs
10281	3.8	R80333	Hs.21182	ESTs
25284	3.8	AA045074	Hs.110146	\Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]
6730	3.8	Y09305	Hs.17154	H.sapiens mRNA for protein kinase Dyrk4 partial
16033	3.8	UMISGF3AM97935	Hs.110832	AFFX-HUIMISGF3AM97935_MB
39242	3.8	AA621523	ESTs	

**FIG.-3Bn**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27354	3.8	AA425221	Hs.81688	ESTs
4552	3.8	U49188	Hs.76329	Human placenta (Diff33) mRNA complete cds
18385	3.8	AA227219	Hs.110826	Homo sapiens CAGF9 mRNA partial cds
16754	3.8	AA046067		EST - RC_AA046067
12752	3.8	AA421250	Hs.4310	ESTs
42463	3.8	W60180	Hs.103135	ESTs
10614	3.8	AA037357	Hs.18045	ESTs
867	3.7	D87716	Hs.90315	Human mRNA for KIAA0007 gene partial cds
7608	3.7	AA180967	Hs.85432	ESTs
31795	3.7	N80703	Hs.50473	ESTs
35377	3.7	AA399453		EST - RC_AA399453
22828	3.7	R98192	Hs.35828	ESTs
25240	3.7	AA039713	Hs.110406	ESTs
11008	3.7	AA134289	Hs.15423	ESTs Weakly similar to ASH1 [D.melanogaster]
4341	3.7	U38545	Hs.82587	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA complete cds
28833	3.7	D59787	Hs.39457	EST - RC_D59787_f
3750	3.7	U09279	Hs.64691	Collagen type XIX alpha 1
17483	3.7	AA122147	Hs.71622	ESTs
16854	3.7	AA055552	Hs.1197	ESTs Weakly similar to KIAA0319 [H.sapiens]
3709	3.7	U07550	Hs.111758	Heat shock 10 kD protein 1 (chaperonin 10)
1608	3.7	L00205	Hs.43107	KERATIN TYPE II CYTOSKELETAL 6D
24577	3.7	Z38727	Hs.91625	Homo sapiens mRNA for KIAA0555 protein complete cds
31032	3.7	N62508	Hs.82321	ESTs
4951	3.7	U69546	Hs.99519	Human RNA binding protein Etr-3 mRNA complete cds
37660	3.7	AA460225	Hs.32170	ESTs
20418	3.6	N49209		ESTs

**FIG.-3Bo**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27995	3.6	AA470155	Hs.75887	Homo sapiens coatomer protein (COPA) mRNA complete cds
7971	3.6	AA287423	Hs.126389	ESTs
27606	3.6	AA443793	Hs.94761	ESTs
24677	3.6	Z39338	Hs.21201	ESTs Highly similar to POLYVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]
11070	3.6	AA148521	Hs.6759	ESTs Weakly similar to putative p150 [H.sapiens]
9328	3.6	D89618	Hs.3886	Homo sapiens importin-alpha homolog (SRP19gamma) mRNA complete cds
36826	3.6	AA435996	Hs.98857	ESTs
17678	3.6	AA134275	Hs.134510	Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3
36209	3.6	AA421266	Hs.13889	ESTs Weakly similar to LIS-1 protein [H.sapiens]
34120	3.6	AA211615	Hs.104173	EST
38152	3.6	AA486737	Hs.105465	H.sapiens mRNA for Sm protein F
38463	3.6	AA504491	Hs.30154	ESTs Weakly similar to contains similarity to C3HC4-class zinc finger [C.elegans]
20064	3.6	H98653	Hs.16056	ESTs
31256	3.6	N66152	Hs.49132	EST
9713	3.6	L44338	Hs.78494	Homo sapiens mRNA for KIAA0525 protein partial cds
28622	3.6	D11837	Hs.29846	ESTs
38057	3.6	AA481549	EST .. RC_AA481549	
28763	3.6	D45568	Hs.65557	EST
16996	3.6	AA069038	EST .. RC_AA069038	
28628	3.6	D11888	Hs.62386	ESTs Moderately similar to PROHIBITIN [H.sapiens]
25804	3.5	AA148885	Hs.111710	ESTs
2492	3.5	M22898	Hs.1846	Tumcr protein p53 (Li-Fraumeni syndrome)
14904	3.5	T83389	Hs.107147	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]

**FIG.\_3Bp**

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FIG.-3Bq

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25585 34018	3.4 3.4	AA112389 AA191488	Hs.107932 Hs.73614	H4(D1(S170)) mRNA Human high-affinity copper uptake protein (HCTR1) mRNA complete cds
251 3778	3.4 3.4	D14520 U09848	Hs.84728 Hs.363	Basic transcription element binding protein 2 Zinc finger protein 139 (clone pHZ-37)
24535	3.4	Z38409	Hs.8053	ESTs
16858	3.4	AA055759	Hs.90998	Human mRNA for KIAA0128 gene partial cds
16127	3.4	AA004669	Hs.39441	ESTs
36683	3.4	AA432268	Hs.104910	ESTs
26149	3.4	AA250824	Hs.60478	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
4011	3.4	U20536	Hs.3280	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds
41001 5660	3.4 3.4	N78844 X16396	Hs.3749 Hs.37791	ESTs ESTs
19204 42323	3.4 3.4	H11629 T98152	Hs.26790 Hs.79432	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE ESTs Fibrillin 2
26928	3.4	AA342580	Hs.47232	ESTs
20497	3.4	N52565	Hs.36055	ESTs
19226	3.4	H12455	Hs.13026	ESTs
36267	3.4	AA424046	Hs.98385	ESTs
32257	3.4	R54726	Hs.98493	DNA-REPAIR PROTEIN XRCC1
17365	3.4	AA101551	Hs.68900	ESTs
15296	3.3	W16684	Hs.74284	Moderately similar to <i>S.cerevisiae</i> hypothetical protein L3111 [H.sapiens]
17675 40332	3.3 3.3	AA134064 H97565	Hs.44045 Hs.108805	ESTs Homo sapiens mRNA from chromosome 5q21-22 clone:A3-A

FIG.-3Br

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7219	3.3	AA056319	Hs.79326	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds
10006	3.3	N81193	Hs.43133	Homo sapiens mRNA for KIAA0628 protein complete cds
33985	3.3	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
9570	3.3	H85169	Hs.24837	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds
37551	3.3	AA456679	Hs.7256	ESTs
886	3.3	D88613	Hs.28346	Human mRNA for hGCMA complete cds
23650	3.3	T86293	Hs.16144	ESTs
18367	3.3	AA224180	Hs.93332	ESTs Moderately similar to ovarian-specific protein [R. norvegicus]
42494	3.3	W69385	Hs.100002	H.sapiens NumA gene (Clone T33)
14310	3.3	AA598412	Hs.8739	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION [Saccharomyces cerevisiae]
19233	3.3	H12634	Hs.8104	ESTs
42283	3.3	T94343	Hs.31016	Homo sapiens M962 protein spliced isoform 2 mRNA complete cds
12809	3.3	AA424406	Hs.31839	ESTs
36285	3.3	AA424469	Hs.97849	ESTs
21555	3.3	R33073	Hs.24595	EST
13767	3.3	AA463234	Hs.119387	ESTs
4738	3.3	U58766	Hs.75801	Human FX protein mRNA complete cds
7258	3.3	AA075427	Hs.17296	ESTs
17041	3.3	AA070364	EST - RC_AA070364	
15504	3.3	W28362	Hs.44131	ESTs
23793	3.3	T90971	EST - RC_T90971	

**FIG.-3Bs**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18214 7401	3.3 3.3	AA196635 AA094800	Hs.86081 Hs.55682	ESTs Human translation initiation factor eIF3 p66 subunit mRNA complete cds
18912	3.3	F10913	Hs.12475	Homo sapiens clone 23617 unknown mRNA partial cds
36317	3.3	AA425089	HS.50722	Human mRNA for KIAA0334 gene complete cds
9410	3.3	H20443	HS.31748	H.sapiens mRNA for TRE5
21446	3.2	L41390	EST - L41390	
18683	3.2	F04258	HS.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
33891 14435	3.2 3.2	HUMTFR/M11507 AA608730	HS.4192	AFFX-HUMTFR/M11507_M ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA [Garcia intestinalis]
9584	3.2	H88128	HS.41127	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]
22061 35796	3.2 3.2	R49216 AA410223	HS.24984 EST - RC_AA410223	ESTs
37403	3.2	AA453613	HS.128708	ESTs
15796	3.2	X16889	HS.69089	ALPHA-GALACTOSIDASE A PRECURSOR
15840	3.2	X70944	HS.91379	PTB-ASSOCIATED SPLICING FACTOR
7518	3.2	AA147144	EST - AA147144	
32335	3.2	R78248	HS.109156	ESTs
3256	3.2	M92439	HS.87157	130 KD LEUCINE-RICH PROTEIN
4400	3.2	U41387	HS.51122	Human Gu protein mRNA partial cds
7681	3.2	AA206983	HS.104135	Homo sapiens mRNA for DRIM protein
15676	3.2	W68649	HS.9656	ESTs
39590	3.2	F09281	HS.106981	ESTs
26883	3.2	AA291921	HS.44107	ESTs Weakly similar to putative p150 [H.sapiens]

**FIG.\_3Bt**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9808	3.2	M80627	Hs.21704	Transcription factor 12 (HTF4 helix-loop-helix transcription factors 4)
27755	3.2	AA453444 N26011	Hs.6809 Hs.53810	ESTs ESTs
29983	3.2	R15846	Hs.21738	ESTs
21350	3.2	AA280928	Hs.24287	ESTs
11981	3.2	T96690	Hs.125123	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
23930	3.2			EST
30399	3.2	N45226 R59312	Hs.46495 Hs.26641	EST ESTs
22286	3.2	AA453431	Hs.21043	ESTs
13494	3.2	AA427579	Hs.9347	ESTs
12908	3.2	R60567	Hs.26787	ESTs
22319	3.1	N66818	Hs.42179	ESTs
31309	3.1	N64406	Hs.54174	ESTs
31192	3.1	AA196512	Hs.25916	ESTs
11288	3.1	D00596	Hs.82962	Thymidylate synthase
170	3.1	U90549	Hs.63272	Human non-histone chromosomal protein (NHC) mRNA complete cds
5307	3.1			complete cds
26105	3.1	AA243133	Hs.48915	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds
11659	3.1	AA251909 H10984	Hs.36708 Hs.12338	Homo sapiens MAD3-like protein kinase mRNA complete cds
19177	3.1	AA425230	Hs.112013	ESTs
8389	3.1	AA205125	Hs.1087	Protein serine/threonine kinase <i>stk2</i>
34087	3.1	AA004718	Hs.138349	ESTs Weakly similar to BAP31 protein [H.sapiens]
25001	3.1	AA489665	Hs.25245	ESTs
14149	3.1			

FIG.-3Bu

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE ACCESSION	UNIGENE DESCRIPTOR
10167	3.1	R55076	Hs.106645	ESTs
17380	3.1	AA102566	Hs.69149	ESTs
42397	3.1	W42928	Hs.103046	ESTs
14935	3.1	T94828	Hs.63220	ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]
41673	3.1	R78618	Hs.101571	ESTs Weakly similar to GTP-binding protein rab10 [R.no'vegicus]
2750	3.1	M35999	Hs.87149	Integrin beta 3 (platelet glycoprotein IIIa antigen CD61)
3190	3.1	M86808	Hs.131361	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA
17406	3.1	AA112979	Hs.48269	SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR
598	3.1	D59253	Hs.3709	Homc sapiens mRNA for VRK1 complete cds Homc sapiens mRNA for low molecular mass ubiquinone- binding protein complete cds
29348	3.1	H69021	Hs.62394	ESTs
14130	3.1	AA489041	Hs.15140	ESTs
14134	3.1	AA489080	Hs.3566	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]
42421	3.1	W45491	Hs.106835	ESTs Weakly similar to T23G11.7 [C.elegans]
15723	3.1	W79060	Hs.53337	ESTs Highly similar to ribosome-binding protein p34 [R.no'vegicus]
11140	3.1	AA158132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
28531	3.1	C20679	Hs.32753	ESTs
2021	3.1	L34409	Hs.94799	Homc Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14522	3.1	AA610108	Hs.27693	ESTs   highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schizosaccharomyces pombe]
29853	3.1	N22162	Hs.43100	ESTs
15962	3.1	Z21420	Hs.30819	ESTs
6541	3.1	X95632	Hs.86870	Human Abl interactor 2 (Abi-2) mRNA complete cds
13229	3.0	AA443811	Hs.23363	ESTs
27315	3.0	AA424038	Hs.58197	ESTs
13621	3.0	AA456821	Hs.6823	ESTs   highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
35929	3.0	AA412429	Hs.48642	ESTs
17925	3.0	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein Gyr-tbp (GRY-3BP) mRNA complete cds
5053	3.0	U76992	Hs.71134	Human Tat-SF1 mRNA complete cds
15060	3.0	U54999	Hs.93121	Human LGN protein mRNA complete cds
17757	3.0	AA147224	Hs.71814	EST
19050	3.0	H05509	Hs.24639	ESTs
26530	3.0	AA278650	Hs.73291	ESTs
16806	3.0	AA053258	Hs.31921	Homo sapiens mRNA for KIAA0648 protein partial cds
29088	3.0	F13700	Hs.115823	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene :complete cds
22960	3.0	T10272	Hs.4287	ESTs
33585	3.0	W93000	Hs.59389	ESTs
220	3.0	D13627	Hs.84021	Human mRNA for KIAA0002 gene complete cds
4298	3.0	U36448	Hs.74574	Human Ca2+-dependent activator protein for secretion mRNA complete cds
7445	3.0	AA104023	Hs.110048	ESTs

**FIG.-3BW**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40903	3.0	N68670	Hs.103808	ESTs
18055	3.0	AA179387	Hs.73596	ESTs
7282	3.0	AA083339	Hs.126781	ESTs
9348	3.0	H03686	Hs.112013	ESTs
806	3.0	D87009	Hs.43834	Human (lambda) DNA for immunoglobulin light chain
38447	3.0	AA504255	Hs.54404	Human protein kinase ATR mRNA complete cds
41464	3.0	R46837	Hs.107450	ESTs
9662	3.0	L19161	Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
16976	3.0	AA063625	Hs.66696	EST
37426	3.0	AA454016	Hs.99306	ESTs
2588	3.0	M27878	Hs.9450	Zinc finger protein 84 (HPF2)
15174	3.0	U82987	Hs.87246	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds
33620	3.0	W93943	Hs.59509	ESTs
6784	3.0	Y11681	Homo sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds	Hs.9964
41077	3.0	N95028	Hs.125031	ESTs
1932	3.0	L24804	Hs.75839	Human (p23) mRNA complete cds-
39556	3.0	F03738	Hs.3657	ESTs
16108	3.0	AA002258	Hs.59939	ESTs
32156	3.0	R40381	Hs.142852	ESTs
13617	3.0	AA456646	Hs.28661	ESTs
11989	3.0	AA281251	Hs.35696	ESTs Weakly similar to trithorax protein trxII [D.melanogaster]
6056	2.9	X68194	Hs.80919	Pantophysin [human keratinocyte line HaCaT mRNA 2106 nt]
15446	2.9	W27374	Hs.5300	Homo sapiens 10kD protein (BC10) mRNA complete cds
38086	2.9	AA482557	Hs.105139	EST
13878	2.9	AA476604	Hs.7114	ESTs
6209	2.9	X76770	Hs.49007	H.sapiens PAP mRNA

**FIG.-3BX**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
ACCESSION			
388	2.9	D28791	
1351	2.9	G4755-HT5203	Phosphatidylinositol glycan class A (paroxysmal nocturnal hemoglobinuria)
42624	2.9	W87804	EST HG4755-HT5203
34895	2.9	AA311972	ESTs
20157	2.9	N23393	ESTs
29248	2.9	H52918	ESTs
4893	2.9	U66615	Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA complete cds
10104	2.9	R23855	ESTs
15039	2.9	U46116	Protein tyrosine phosphatase receptor type gamma polypeptide
1605	2.9	L00058	V-myc avian myelocytomatisis viral oncogene homolog
4536	2.9	U48705	Receptor protein-tyrosine kinase EDDR1
10173	2.9	R56678	ESTs Weakly similar to cell division control protein CDC21 [H.sapiens]
26555	2.9	AA279071	ESTs Weakly similar to T08A11.2 [C.elegans]
4401	2.9	U41515	Human deleted in split hand/split foot 1 (DSS1) mRNA complete cds
21009	2.9	N90401	ESTs
3602	2.9	U01317	HEMOGLOBIN EPSILON CHAIN
4833	2.9	U63455	Sulfonylurea receptor (hyperinsulinemia)
36200	2.9	AA421164	ESTs
26645	2.9	AA281076	ESTs
35299	2.9	AA398622	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)
9804	2.9	M74558	Human SII mRNA complete cds
5216	2.9	U83410	Human CUL-2 (cul-2) mRNA complete cds

**FIG.-3By**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12313	2.9	AA397916	Hs.22595	ESTs
5928	2.9	X62048	Hs.75188	WEE1-LIKE PROTEIN KINASE
39586	2.9	F09155	Hs.77822	ESTs
34758	2.9	AA287680	Hs.99676	EST
18199	2.9	AA195318	Hs.63311	ESTs
19867	2.9	H61476	Hs.15641	ESTs
6081	2.9	X69398	Hs.82685	CD47 antigen (Rh-related antigen integrin-associated signal transducer)
5254	2.9	U86782	Hs.76887	Human 26S proteasome-associated-pd1 homolog (POH1) mRNA complete cds
13579	2.9	AA455967	Hs.106705	Human neuronal PAS2 (NPAS2) mRNA complete cds
1117	2.9	HG3075-HT3236	EST - HG3075-HT3236	
20533	2.9	N54407	Hs.34570	ESTs
38495	2.9	AA505118	Hs.112255	Human nucleoporin 98 (NUP98) mRNA complete cds
33729	2.9	Z39654	Hs.65789	EST
20228	2.9	L35035	Hs.79886	RIBO3E 5-PHOSPHATE ISOMERASE
27374	2.9	AA425816	Hs.64641	ESTs Weakly similar to Y53C12A.3 [C.elegans]
19404	2.9	H20568	Hs.27182	ESTs
26108	2.9	AA243189	Hs.53652	ESTs
4189	2.8	U30930	Hs.57700	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
16708	2.8	AA043944	Hs.62663	ESTs
357	2.8	D26156	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
26045	2.8	AA236276	Hs.87287	ESTs
17796	2.8	AA150435	Hs.72063	ESTs
8059	2.8	AA310967	Hs.5080	ESTs Weakly similar to T04A8.11 [C.elegans]

FIG.-3BZ

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40914	2.8	N69220	Hs.41381	ESTs
27169	2.8	AA410287	Hs.90304	H.sapiens mRNA for basic transcription factor 2 34 kD subunit
21358	2.8	R16079	Hs.14775	ESTs
3572	2.8	S87759	Hs.57764	Protein phosphatase 2C alpha [human teratocarcinoma mRNA 2346 nt]
11877	2.8	AA262727	Hs.9591	ESTs
1653	2.8	L05424	Hs.57649	CD44 antigen (cell adhesion molecule)
24645	2.8	Z39106	Hs.92414	ESTs
35830	2.8	AA411448	Hs.139386	ESTs
4433	2.8	U43279	EST - U43279	
20151	2.8	N22895	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA partial cds
38648	2.8	AA599267	EST - RC_AA599267	
7777	2.8	AA236820	Hs.118236	ESTs
32845	2.8	W31566	Hs.55459	EST
28258	2.8	AA505133	Hs.62273	ESTs
6853	2.8	Z22951	Hs.75569	TRANSCRIPTION FACTOR P65
35944	2.8	AA412488	Hs.98150	ESTs
30648	2.8	N50971	Hs.42116	ESTs
18965	2.8	H01411	Hs.24382	ESTs
86116	2.8	AA460077	Hs.28555	ESTs
14945	2.8	T99606	Hs.11085	ESTs Weakly similar to F35G2.2 [C.elegans]
8375	2.8	AA422160	Hs.103144	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds
34929	2.8	AA342084	EST - RC_AA342084	
326	2.8	D21262	Hs.75337	Human mRNA for KIAA0035 gene partial cds
27057	2.8	AA400998	Hs.49559	ESTs
36292	2.8	AA424513	EST - RC_AA424513	

FIG.-3Ca

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
6480	2.8	X91788 W27054 AA243007	Hs.84974 Hs.1255 Hs.16420	H.sapiens mRNA for Ichn protein APOLIPOPROTEIN AI REGULATORY PROTEIN-1
15424	2.8	AA194730 AA034527	Hs.85916 Hs.95182	ESTs EST
11602	2.8	L07493	Hs.1608	Replication protein A (E coli RecA homolog RAD51 homolog)
18175	2.8	AA621122 AA115769 AA490885	Hs.5198 Hs.142290 Hs.21766	ESTs ESTs ESTs
25202	2.8	N72196	Hs.50199	EST
1681	2.8	AA206370	Hs.86248	Regulatory factor (trans-acting) 3
14566	2.8	X76092	Hs.38841	ESTs
25614	2.8	T03865	Hs.27047	Homo sapiens RRM RNA binding protein GRY-RBP (GRY-RBP)
14182	2.8	AA401274	Hs.31730	mRNA, complete cds
31599	2.8			mRNA, Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH
18253	2.7			[R.norvegicus]
6193	2.7			ESTs (Moderately similar to C-1-TETRAHYDROFOLATE)
22911	2.7			SYNT-HASE CYTOPLASMIC [H.sapiens]
35549	2.7			Human retinoblastoma-binding protein (RbAp46) mRNA
35955	2.7	AA412528	Hs.20183	complete cds
17642	2.7	AA132983	Hs.44155	ESTs
6131	2.7	X72841	Hs.2758	EST - RC_AA070815
				ESTs
41429	2.7	R44994 AA070815 AA235050	Hs.108182 Hs.142190	EST
17052	2.7	T10065	Hs.4214	Homo sapiens TLS-associated protein TASR-2 mRNA
34243	2.7			complete cds
22937	2.7			

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5183	2.7	U82130	Hs.118910	Human tumor susceptibility protein (TSG101) mRNA complete cds
30837	2.7	N54416	Hs.47820	ESTs
16243	2.7	AA012902	Hs.60556	ESTs
19954	2.7	H80100	Hs.33977	ESTs
6444	2.7	X89750	Hs.90077	H.sapiens mRNA for TGIF protein
5916	2.7	X61072	Hs.99996	Human mRNA for T cell receptor clone IGRA17
6240	2.7	X78627	Hs.75066	H.sapiens mRNA for translin
42116	2.7	T69924	EST - RC_T69924	
7701	2.7	AA215333	Hs.97101	ESTs
17568	2.7	AA128905	Hs.22587	ESTs
42534	2.7	W73189	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
29813	2.7	N21111	Hs.42946	ESTs
38898	2.7	AA609458	Hs.98265	ESTs
10316	2.7	R88880	Hs.107823	ESTs Moderately similar to zinc finger protein [M.musculus]
14769	2.7	S54641	Hs.73103	HZF-16
32961	2.7	W38366	Hs.77493	Human mRNA for KIAA0005 gene complete cds
35273	2.7	AA398507	Hs.97361	ESTs
10180	2.7	R60100	Hs.25986	ESTs
32563	2.7	T27697	Hs.21603	Human mRNA for KIAA0036 gene complete cds
34502	2.7	AA262768	Hs.7523	ESTs
13223	2.7	AA443720	Hs.7551	ESTs
8494	2.7	AA443460	Hs.3430	ESTs
7776	2.7	AA236771	Hs.101368	ESTs
10400	2.7	AA007234	Hs.30098	ESTs
1130	2.7	G3132-HT3308	EST - HG3132-HT3308	

FIG.-3Cc

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2379 18906	2.7 2.7	M16937 F10868	Hs.819 Hs.46571	Human homeo box c1 protein mRNA complete cds Human SH3 domain-containing protein SH3P18 mRNA complete cds
34796	2.7	AA291259	Hs.97101	ESTs
41955	2.7	T33311	Hs.3281	Neuronal pentraxin II
2009	2.7	L33881	Hs.1904	Protein kinase C iota
33688	2.7	Z38501	Hs.8768	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]
1385	2.7	G884-HT884	EST - HG884-HT884	
24758	2.7	Z40075	Hs.27596	ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE
7620	2.7	AA192484	Hs.62669	PROTEASE SUBUNIT 2 [S.cerevisiae]
30733	2.7	N52078	Hs.13604	Homo sapiens mRNA for KIAA0637 protein complete cds
21256	2.7	R09195	Hs.86013	Homo sapiens mRNA for KIAA0564 protein partial cds
40528	2.7	N29325	Hs.107914	ESTs Highly similar to 47 KD PROTEIN [Pseudomonas chlororaphis]
25285	2.7	AA045083	Hs.77719	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE
9296	2.7	D82775	Hs.10724	ESTs Weakly similar to unknown [S.cerevisiae]
12174	2.7	AA292128	Hs.26750	ESTs
38357	2.7	AA491265	Hs.105285	EST
3154	2.7	M83712	Hs.1614	Cholinergic receptor nicotinic alpha polypeptide 5
7383	2.7	AA093834	Hs.109822	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S.cerevisiae]
1923	2.7	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage elastase)
24906	2.7	Z41840	Hs.8817	ESTs
30407	2.6	N45983	Hs.46572	ESTs
34726	2.6	AA287278	Hs.97721	ESTs

FIG.\_3Cd

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
			UNIGENE CLUSTER	UNIGENE SC WARNING
20408	2.6	N48787	Hs.28378	ESTs Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]
7158	2.6	AA037206	Hs.72071	ESTs
26286	2.6	AA253351	Hs.44439	ESTs
19822	2.6	H58684	Hs.37573	ESTs
12379	2.6	AA399418	Hs.23170	Homo sapiens mRNA for JM23 protein complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))
22698	2.6	R89287	Hs.29406	ESTs
24161	2.6	W58015	Hs.34820	ESTs
9558	2.6	H81497	Hs.12063	ESTs
18104	2.6	AA188801	Hs.85634	ESTs
24882	2.6	Z41563	Hs.26975	ESTs
40038	2.6	H69485	Hs.8236	ESTs
8865	2.6	AB002359	Hs.105478	Human mRNA for KIAA0361 gene KIAA0361 protein
22148	2.6	R51831	Hs.25829	ESTs
4627	2.6	U51990	Hs.94178	Human hPrp18 mRNA complete cds
8394	2.6	AA426156	Hs.42714	ESTs
20422	2.6	N49300	Hs.24908	ESTs
41602	2.6	R67258	HS.58215	Moderately similar to rhotekin [M.musculus]
612	2.6	D63480	Hs.74670	Human mRNA for KIAA0146 gene partial cds
4821	2.6	U62801	Hs.79361	Human protease M mRNA complete cds
16807	2.6	AA053296	Hs.63136	ESTs
15288	2.6	W07562	Hs.26198	ESTs Moderately similar to rA8 [R.norvegicus]
38023	2.6	AA481066	Hs.105153	ESTs

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23822	2.6	T91715	Hs.14574	ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]
10951	2.6	AA126719	Hs.25282	ESTs RETINOBLASTOMA BINDING PROTEIN P48
6150	2.6	X74262	Hs.81058	ESTs Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]
39336	2.6	C20945	Hs.108117	ESTs Highly similar to modulator recognition factor 2 [H.sapiens]
			Hs.71587	ESTs
			Hs.93667	Homo sapiens Ly-9 mRNA complete cds
			Hs.83062	Human Chromosome 16 BAC clone C1T987SK-A-270G1
			Hs.110103	Human C-1 mRNA complete cds
			Hs.91161	Homo sapiens chromosome 19 cosmid R30783
			Hs.70830	Homo sapiens mRNA for SCP-1 complete cds
			Hs.112743	ESTs
			Hs.83313	ESTs
			Hs.27842	Human antisecretory factor-1 mRNA complete cds
			Hs.111709	EST - ITC_AA598938
				ESTs
				Hs.32471
				ESTs
				Hs.110031
				ESTs
				Hs.94217
				U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
				ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME
				E2-17  D [Drosophila melanogaster]
				ESTs
10655	2.6	AA040882	Hs.10290	

FIG.-3Cf

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
	ACCESSION		
14053	2.6	AA485147	Hs.12263 ESTs Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]
31574	2.6	N71303	Hs.50015 EST
7614	2.6	AA187579	Hs.102696 ESTs Weakly similar to Yel007c-ap [S.cerevisiae]
37971	2.6	AA479195	Hs.105620 EST
7090	2.6	AA009913	Hs.103300 Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds
17852	2.6	AA156360	Hs.54823 ESTs
24219	2.6	W69960	Hs.19416 ESTs
19070	2.6	H05970	Hs.133828 Human clone 23960 mRNA sequence
17719	2.6	AA136569	Hs.144295 EST
38669	2.6	AA599694	Hs.57730 Human mRNA for KIAA0133 gene complete cds
20982	2.6	N79565	Hs.29894 ESTs
9158	2.6	D31446	Hs.10488 Homo sapiens breakpoint cluster region protein 1 (BCRG1) mRNA complete cds
11362	2.6	AA227261	Hs.20922 ESTs
8613	2.6	AA459555	Hs.31921 Homo sapiens mRNA for KIAA0648 protein partial cds
13866	2.6	AA476319	Hs.5327 ESTs
10303	2.6	R86178	Hs.51187 Ataxia telangiectasia mutated (includes complementation groups A C and D)
22299	2.6	R59601	Hs.26679 EST
18257	2.6	AA206591	EST - FIC_AA206591
20555	2.6	N55168	ESTs
39552	2.6	F03605	PUTATIVE 60S RIBOSOMAL PROTEIN
27530	2.6	AA435999	ESTs
1795	2.6	L13434	Hs.841162 Human chromosome 3p21.1 gene sequence complete cds
14746	2.6	D60354	Hs.90315 Human mRNA for KIAA0007 gene partial cds

**FIG.\_3Cg**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2993	2.6	M64929	Hs.75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52), alpha isoform
19191	2.6	H11297	Hs.31050	ESTs
12986	2.6	AA430032	Hs.7487	ESTs Moderately similar to PTTG gene product [R.norvegicus]
15452	2.5	W27451	Hs.12064	Human Cdc5-related protein (PCDC5RP) mRNA complete cds
18003	2.5	AA171692	Hs.70980	ESTs
24198	2.5	W67524	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
42653	2.5	W92703	Hs.103239	ESTs
26446	2.5	AA258796	Hs.142200	ESTs Weakly similar to putative p150 [H.sapiens]
30438	2.5	N47204	Hs.46680	ESTs Weakly similar to C50F4.12 [C.elegans]
36365	2.5	AA425893	Hs.26676	ESTs Weakly similar to probable CBP3 protein homolog [C.elegans]
26135	2.5	AA243765	Hs.76977	ESTs
41885	2.5	T23449	Hs.110218	ESTs Moderately similar to ZNF127-Xp [H.sapiens]
15457	2.5	W27560	Hs.90789	ESTs
27748	2.5	AA453159	Hs.41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
32315	2.5	R69840	Hs.70189	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]
25310	2.5	AA046745	Hs.110457	ESTs
42720	2.5	Z39436	Hs.102720	ESTs
12939	2.5	AA428204	Hs.22630	ESTs
30746	2.5	N52243	Hs.47435	ESTs
22222	2.5	L76703	Hs.79326	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds
11609	2.5	AA243303	Hs.21187	ESTs

**FIG.-3Ch**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9658	2.5	L16991	Hs.79006	Deoxythymidylate kinase
12210	2.5	AA293774	Hs.21261	ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL [C.elegans]
3563	2.5	S83364	EST - S833364	
42407	2.5	W44768	Hs.75474	Homo sapiens nephrocystin (NPHP1) mRNA partial cds
32826	2.5	W20391	Hs.20830	Human mRNA for kinesin-related protein partial cds
9692	2.5	L37747	Hs.89497	LAMIN B1
27862	2.5	AA458908	ESTs	
33691	2.5	Z38630	Hs.50883	
17288	2.5	AA085178	Hs.56901	EST
9883	2.5	N35449	Hs.24382	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]
5932	2.5	X62153	Hs.82479	Minichromosome maintenance deficient (S. cerevisiae) 3
15885	2.5	X95073	Hs.96247	H.sapiens mRNA for translin associated protein X
17952	2.5	AA165677	Hs.65757	ESTs Weakly similar to F16A11.1 [C.elegans]
12197	2.5	AA293206	Hs.10852	
6210	2.5	X76942	Hs.77335	Homo sapiens golgin-245 mRNA complete cds
34047	2.5	AA194166	Hs.106928	ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]
16929	2.5	AA058952	Hs.62590	ESTs
26834	2.5	AA287138	Hs.59346	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE
5157	2.5	U80034	Hs.68583	[Thermus aquaticus thermophilus] Human mitochondrial intermediate peptidase precursor (MIEP) mRNA mitochondrial gene encoding mitochondrial protein
38434	2.5	AA497013	Hs.142592	mRNA mitochondrial complete cds
			ESTs	

**FIG.\_3Ci**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33269	2.5	W72967	Hs.58257	ESTs
26991	2.5	AA398284	Hs.48050	ESTs
7590	2.5	AA173505	Hs.35353	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHC2-POL3 INTERGENIC REGION [S.cerevisiae]
14960	2.5	U05237	Hs.99872	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds
13585	2.5	AA455999	Hs.22151	ESTs Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]
35901	2.5	AA412151	Hs.108974	ESTs
38185	2.5	AA487508	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
34678	2.5	AA284744	Hs.75510	Annexin XI (56kD autoantigen)
1424	2.5	J02645	Hs.81613	Eukaryotic translation initiation factor 2A
16778	2.5	AA047008	Hs.62800	ESTs
21876	2.5	R43286	EST - RC_R43286	
17779	2.5	AA149641	Hs.55405	ESTs
24559	2.5	Z38588	Hs.7988	ESTs
7781	2.5	AA242904	Hs.40637	Homo sapiens proline-rich Gla protein 1 (PRGP1) mRNA complete cds
7474	2.5	AA126592	Hs.5400	ESTs Weakly similar to No definition line found [C.elegans]
34290	2.5	AA236866	Hs.111314	ESTs
5316	2.5	U90905	Hs.79385	Human clone 23574 mRNA sequence
10218	2.5	R68884	Hs.86347	ESTs Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCC2-MRF1 INTERGENIC REGION [Saccharomyces cerevisiae]
18109	2.5	AA188981	Hs.58169	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds
6485	2.5	X92098	Hs.75914	H.sapiens mRNA for transmembrane protein rnp24

**FIG.-3Cj**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34954	2.5	AA342959	Hs.110041	EST - RC_AA342959
42558	2.5	W74751	ESTs	
27444	2.5	AA430160	Hs.42785	ESTs Weakly similar to F25H9.7 [C.elegans]
21284	2.5	R10301	Hs.20584	EST
8920	2.5	AF006265	Hs.9222	Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds
30037	2.5	N27439	Hs.51652	ESTs
27602	2.5	AA443702	Hs.29835	ESTs Weakly similar to W02B12.7 [C.elegans]
3390	2.5	S59184	Hs.79350	RYK receptor-like tyrosine kinase
25040	2.5	AA010188	Hs.103305	ESTs
37713	2.4	AA461317	Hs.34950	
40477	2.4	N24006	Hs.99348	Homo sapiens BAC clone RG300E22 from 7q21-q31.1
29382	2.4	H72914	Hs.103318	ESTs
35521	2.4	AA400831	Hs.111916	ESTs
20324	2.4	N35406	Hs.74014	Phospholipase C beta 4
18620	2.4	F02506	Hs.9417	ESTs
21087	2.4	R00186	Hs.18866	EST
9950	2.4	N71503	Hs.43087	ESTs
31965	2.4	N93629	Hs.93391	ESTs
15120	2.4	U73524	Hs.87465	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds
28813	2.4	D59257	Hs.91161	Human C-1 mRNA complete cds
38082	2.4	AA482284	Hs.110493	ESTs
34723	2.4	AA287115	Hs.99697	ESTs
7960	2.4	AA285277	Hs.8932	Homo sapiens brain expressed ring finger protein mRNA complete cds
18073	2.4	AA180453	Hs.73643	EST

**FIG.-3Ck**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36755	2.4	AA435698		EST - RC_AA435698
18927	2.4	F11087	Hs.12544	ESTs
3457	2.4	S74728	Hs.74294	Antiquitin
38606	2.4	AA598844	Hs.112492	ESTs
20967	2.4	N76086	Hs.35464	
24752	2.4	Z40012	Hs.21862	Homo sapiens mRNA for KIAA0587 protein complete cds
28443	2.4	AA621611	Hs.70877	ESTs
452	2.4	D38076	Hs.24763	RAN binding protein 1
11701	2.4	AA253031	Hs.31730	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds
13655	2.4	AA458919	Hs.30212	ESTs Weakly similar to 26S proteasome subunit p44.5 [H.sapiens]
24822	2.4	Z40956	Hs.111541	ESTs
12672	2.4	AA417067	Hs.13055	ESTs
4836	2.4	U63717	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
42200	2.4	T83729		EST - RC_T83729
10987	2.4	AA132239	Hs.11810	ESTs Highly similar to HYPOTHETICAL 47.4 KD PROTEIN IN SHF1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]
35672	2.4	AA404995		EST - RC_AA404995
6224	2.4	X77748	Hs.3786	Glutamate receptor metabotropic 3
28395	2.4	AA610064	Hs.73602	ESTs
36390	2.4	AA4426291	Hs.108527	ESTs Weakly similar to No definition line found [C.elegans]
21045	2.4	N93403	Hs.109441	ESTs
4558	2.4	U49379	Hs.54506	Human diacylglycerol kinase epsilon DGK mRNA complete cds
12916	2.4	AA427745	Hs.37747	ESTs

**FIG.-3Cl**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20850	2.4	N69514	Hs.28877	ESTs Weakly similar to oxidoreductase [H.sapiens]
29759	2.4	H99972	Hs.42771	ESTs
36786	2.4	AA435815	Hs.77965	Human Cik-associated RS cyclophilin CARS-Cyp mRNA complete cds
31942	2.4	N93185	Hs.54911	ESTs
7097	2.4	AA011452	Hs.21840	ESTs
39462	2.4	D60063	Hs.9012	ESTs
14420	2.4	AA600322	Hs.19574	ESTs Highly similar to AAC-RICH mRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum] EST - RC_AA282527
34629	2.4	AA282527	Hs.40541	ESTs
27431	2.4	AA429038	Hs.105465	H.sapiens mRNA for Sm protein F
6387	2.4	X85372	Hs.14843	Homo sapiens mRNA for KIAA0704 protein partial cds
11342	2.4	AA223874	Hs.3378	Topoisomerase (DNA) II alpha (170kD)
1497	2.4	J04088	Hs.95723	Centromere autoantigen C
9841	2.4	M95724	Hs.23348	ESTs
11454	2.4	AA233854	Hs.88245	Homo sapiens mRNA for E1B-55kDa-associated protein
29950	2.4	N24902	Hs.104613	ESTs Weakly similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]
8396	2.4	AA426176	Hs.1098	Human terminal transferase mRNA complete cds
32978	2.4	W42788	Hs.48855	ESTs
27872	2.4	AA459254	Hs.31082	ESTs
11623	2.4	AA243617	Hs.88663	ESTs
26582	2.4	AA279768	Hs.124275	Homo sapiens mRNA for KIAA0659 protein partial cds
22142	2.4	R51382	Hs.38114	ESTs Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]
13533	2.4	AA454607	Hs.6145	ESTs
11534	2.4	AA236223		

**FIG.-3Cm**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5976	2.4	X64229	Hs.110713	DEK PROTEIN
6231	2.4	X78121	Hs.2010	Choroideremia
2382	2.4	M16967	Hs.30054	Coagulation factor V
22887	2.4	TG3314	Hs.25402	ESTs
24371	2.4	W87415	Hs.16918	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
25286	2.4	AA045261	Hs.108259	ESTs
9054	2.4	C02472	Hs.5151	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]
8163	2.4	AA357394	Hs.98073	ESTs
12233	2.4	AA343513	Hs.28813	ESTs Weakly similar to LINE/Ig H-chain fusion protein [M.musculus]
22924	2.4	T08195	Hs.37772	ESTs
14371	2.4	AA599219	Hs.30272	Moderately similar to ALR [H.sapiens]
12401	2.4	AA400229	Hs.30503	ESTs
26169	2.4	AA251089	Hs.94576	ESTs Weakly similar to ORF YOR281c [S.cerevisiae]
23065	2.4	T23539	Hs.7165	ESTs Highly similar to zinc finger protein [M.musculus]
20524	2.4	N53965	Hs.15741	ESTs
20837	2.4	N69263	Hs.20524	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]
18201	2.4	AA195398	Hs.144550	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1 the ADORA2BP adenosine A2b receptor LIKE pseudogene the IRF6
7813	2.4	AA248297	Hs.72805	ESTs
21195	2.4	R07710	Hs.19913	ESTs
13377	2.4	AA449720	Hs.20201	Homo sapiens clone 24706 mRNA sequence
9714	2.3	L44367	Hs.86523	ESTs

*FIG.\_3Cn*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41537	2.3	R55673	Hs.106627	ESTs
17352	2.3	AA100925	Hs.20990	ESTs
11914	2.3	AA278907	Hs.24549	ESTs
24890	2.3	Z41634	Hs.26037	ESTs
28796	2.3	D51272	EST - RC_D51272_s	
36798	2.3	AA435870	Hs.97574	ESTs Weakly similar to B0564.1 [C.elegans]
22491	2.3	R70012	Hs.29055	EST
4798	2.3	U61538	Hs.85301	Human calcium-binding protein chp mRNA complete cds
40847	2.3	N66354	Hs.109437	ESTs
15657	2.3	W63627	Hs.141503	Small inducible cytokine A5 (RANTES)
24482	2.3	Z38137	Hs.15386	ESTs
42022	2.3	T53138	Hs.19582	Homo sapiens mRNA for hTCF-4
38233	2.3	AA489023	Hs.99807	ESTs
41221	2.3	R21531	Hs.78973	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
8053	2.3	AA309880	Hs.109957	ESTs
363	2.3	D26528	Hs.123058	Human mRNA for RNA helicase complete cds
26679	2.3	AA281733	Hs.4310	ESTs
13407	2.3	AA450200	Hs.7919	ESTs
17955	2.3	AA166703	Hs.93589	ESTs
31858	2.3	N90680	Hs.54642	EST
24092	2.3	W42845	Hs.14611	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
16759	2.3	AA046294	Hs.40814	ESTs
7861	2.3	AA252436	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
41176	2.3	R09379	Hs.57435	Natural resistance-associated macrophage protein 2

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
3860	2.3	U13913	Hs.89463	Homolog of Drosophila slowpoke (potassium channel calcium-activated)
40886	2.3	N68149	Hs.5151	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]
19428	2.3	H22949	Hs.31942	EST
36080	2.3	AA417282	EST - FIC_AA417282	
27264	2.3	AA418389	Hs.42219	ESTs
13600	2.3	AA456286	Hs.30794	ESTs
13552	2.3	AA454943	Hs.29911	ESTs
15664	2.3	W67456	Hs.56936	ESTs Moderately similar to YY1-associated factor 2 [H.sapiens]
26583	2.3	AA279774	Hs.142497	ESTs
37434	2.3	AA454149	Hs.99357	EST
7833	2.3	AA249300	Hs.7048	ESTs
3674	2.3	U05237	Hs.99872	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds
33694	2.3	Z38770	Hs.711623	ESTs
11178	2.3	AA167436	Hs.20848	ESTs
16977	2.3	AA064616	Hs.66983	ESTs
19799	2.3	H57330	Hs.37430	EST
5948	2.3	X63337	EST - X63337	
42097	2.3	T66318	Hs.78770	Isoleucine-tRNA synthetase
24247	2.3	W73010	Hs.108761	Ribosomal protein L37
40879	2.3	N67816	Hs.53263	ESTs Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]
5875	2.3	X59405	Hs.83532	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)
22325	2.3	R60777	Hs.8358	ESTs

**FIG.\_3Cp**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9621	2.3	J05032	Hs.80758	ASPARTYL-TRNA SYNTHETASE
9239	2.3	D79100	Hs.83196	ESTs
41997	2.3	T47788	Hs.109628	ESTs
31105	2.3	N63207	Hs.48735	EST
39565	2.3	F04320	Hs.35120	Replication factor C 37-kD subunit
7404	2.3	AA094989	Hs.7381	Homo sapiens voltage dependent anion channel protein mRNA :complete cds
6388	2.3	X85373	Hs.77496	H.sapiens mRNA for Sm protein G
20263	2.3	N31952	Hs.103747	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III [Caenorhabditis elegans]
14529	2.3	AA620307	Hs.27379	ESTs
21197	2.3	R07320	Hs.19936	ESTs
28203	2.3	AA490969	Hs.59838	ESTs
38320	2.3	AA490611	Hs.99838	ESTs
41625	2.3	R69333	Hs.10490	ESTs
4674	2.3	U54999	Hs.93121	Human LGN protein mRNA complete cds
28861	2.3	D80037	Hs.45129	EST Weakly similar to C50B8.3 [C.elegans]
31062	2.3	N62827	Hs.48645	ESTs
26756	2.3	AA283832	Hs.86619	Homo sapiens activated protein kinase activated
11567	2.3	AA236747	Hs.30327	protein kinase gene complete cds
25050	2.3	AA011134	Hs.25863	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
26895	2.3	AA292765	Hs.42650	H.sapiens mRNA for M-phase phosphoprotein mpp5
40585	2.3	N34891	Hs.104929	Homo sapiens mRNA for KIAA0595 protein partial cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
3343	2.3	M97936	Hs.21486	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
42435	2.3	W46994	Hs.109903	ESTs
5937	2.2	X62534	Hs.80684	High-mobility group (nonhistone chromosomal) protein 2
21241	2.2	R08617	Hs.20190	ESTs
25756	2.2	AA135868	Hs.95783	ESTs
34184	2.2	AA227959	Hs.3280	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA :complete cds
8672	2.2	AA477046	Hs.59838	ESTs
7387	2.2	AA093977	Hs.71475	ESTs
28822	2.2	D59352	Hs.80624	ESTs
18016	2.2	AA173223	Hs.44426	ESTs
20843	2.2	N69352	Hs.5683	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds
10054	2.2	R10266	Hs.120997	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]
34094	2.2	AA206088	Hs.104139	ESTs
41246	2.2	R27796	Hs.23240	ESTs
22634	2.2	R82837	Hs.103329	ESTs
19686	2.2	H48502	Hs.28212	ESTs
34568	2.2	AA280609	Hs.111288	ESTs Weakly similar to K02B2.3 gene product [C.elegans] Human 26S proteasome-associated pad1 homolog (POH1)
28448	2.2	AA621752	Hs.76887	mRNA :complete cds
20909	2.2	N71704	Hs.4310	ESTs
651	2.2	D78129	EST - D78129	
40409	2.2	H99877	Hs.85951	Homo sapiens exportin t mRNA complete cds

*FIG.\_3Cr*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20340	2.2	N38825	Hs.36958	ESTs
20002	2.2	H93005	EST - FIC_H93005	
37321	2.2	AA451898	Hs.99260	ESTs
8274	2.2	AA402095	Hs.63131	ESTs
20221	2.2	N29345	Hs.28917	ESTs
5792	2.2	X54941	Hs.77550	CDC28 protein kinase 1
4034	2.2	U21858	Hs.60679	Human transcription initiation factor TFIID subunit TAFI131 mRNA;complete cds
36222	2.2	AA421481	Hs.98134	ESTs
16567	2.2	AA031591	Hs.82920	ESTs
4721	2.2	U58046	Hs.82131	Human mRNA for KIAA0139 gene complete cds
28656	2.2	D19708	Hs.5122	Human Gu protein mRNA partial cds
20723	2.2	N66093	Hs.21964	ESTs
6714	2.2	Y08612	Hs.90734	H.sapiens mRNA for Nup88 protein
19240	2.2	H13265	Hs.31196	ESTs
36447	2.2	AA428188	Hs.26006	ESTs
11688	2.2	AA252672	Hs.103300	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA;complete cds
21650	2.2	R37938	Hs.11911	Homo sapiens KIAA0440 mRNA partial cds
14152	2.2	AA489790	Hs.4976	Homo sapiens Ran-GTP binding protein mRNA partial cds
42657	2.2	W92771	Hs.77631	GLYCINIE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
4642	2.2	U52427	Hs.14839	Human RNA polymerase II subunit hsrPB7 mRNA complete cds
32779	2.2	W02102	Hs.53565	ESTs
38341	2.2	AA490967	Hs.105276	ESTs
11803	2.2	AA257971	Hs.21214	ESTs
34835	2.2	AA292677	Hs.80624	ESTs

**FIG.-3Cs**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39085	2.2	AA620599 U22376	Hs.24766 Hs.1334	MYB PROTO-ONCOGENE PROTEIN
4046	2.2	AA242868	Hs.7395	ESTs V/early similar to house-keeping protein [M.musculus]
11600	2.2	U76638	Hs.54089	Human BRCA1-associated RING domain protein (BARD1)
5051	2.2			mRNA complete cds
33917	2.2	AA167323 N63392	Hs.111046 Hs.128003	ESTs
20674	2.2	N91246	Hs.102897	ESTs
41031	2.2	AA020923	Hs.103353	EST
25114	2.2	Z39645	Hs.21470	ESTs
24711	2.2	U58658	Hs.576689	Human unknown protein mRNA within the p53 intron 1 complete cds
4733	2.2			Human glypican-5 (GPC5) mRNA complete cds
4871	2.2	U66033 H99398	Hs.76828 Hs.42680	EST
29733	2.2	T30550	Hs.22615	ESTs
23155	2.2	AA282987	Hs.104473	EST
34638	2.2	AA400986	Hs.99955	Prothrymosin alpha
35541	2.2	L20591	Hs.1378	Annexin III (lipocortin III)
1889	2.2	U68111	Hs.91585	PROTEIN PHOSPHATASE INHIBITOR 2
15106	2.2	H79779	Hs.6975	Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds
40131	2.2			EST
19516	2.2	H29207	Hs.32459	ICH-2 PROTEASE PRECURSOR
4136	2.2	U28014	Hs.74122	ESTs
20276	2.2	N32919	Hs.27931	ESTs Highly similar to 40 KD PROTEIN [Bornavirus]
13292	2.2	AA447621	Hs.31257	ESTs
20666	2.2	N63165	Hs.23618	Sp3 transcription factor
6065	2.2	X68560	Hs.44450	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18238	2.2	AQ205389	Hs.41145	ESTs
21627	2.2	R37410	Hs.21095	EST
3438	2.2	S72024	Hs.119140	Eukaryotic translation initiation factor 5A
34648	2.1	AA283772	Hs.79097	ACTIVATOR 1 36 KD SUBUNIT
5964	2.1	X63657	Hs.74050	Follicular lymphoma variant translocation 1
13250	2.1	AA446459	Hs.27599	ESTs
34370	2.1	AA251829	Hs.104058	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MEF2-CPR7 INTERGENIC REGION [Saccharomyces cerevisiae]
27996	2.1	AA470156	Hs.80449	ESTs Weakly similar to dynein 74K chain cytosolic [R.norvegicus]
4408	2.1	U41745	Hs.8653	Human PDGF associated protein mRNA complete cds
4187	2.1	U30888	Hs.75981	Human tRNA-guanine transglycosylase mRNA complete cds
10804	2.1	AA069549	Hs.18479	ESTs
34552	2.1	AA279985	Hs.18389	Human mRNA for KIAA0372 gene complete cds
18380	2.1	AA227119	Hs.70256	ESTs
5223	2.1	U83843	EST - U83843	
37415	2.1	AA453807	Hs.99349	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]
14582	2.1	AA621340	Hs.10600	ESTs
27756	2.1	AA453447	Hs.59421	ESTs Highly similar to PRE-mRNA SPLICING FACTOR RNA
13787	2.1	AA463745	Hs.122981	HELICASE PRP22 [Saccharomyces cerevisiae]
5173	2.1	U81554	Hs.5171	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40029	2.1	H68221	Hs.10832	Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA complete cds
19972	2.1	H83639	Hs.33576	ESTs
23301	2.1	T52847	Hs.13034	ESTs
20504	2.1	N52966	Hs.142838	ESTs
40145	2.1	H81391	Hs.81182	Human mRNA for histamine N-methyltransferase complete cds
3461	2.1	S75256	EST - S75256	
41893	2.1	T23611	Hs.51251	
39298	2.1	C14805	EST - FIC_C14805	
36021	2.1	AA416876	Hs.5169	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens]
8382	2.1	AA424199	Hs.106529	ESTs Weakly similar to C50B8.3 [C.elegans]
28288	2.1	AA598447	Hs.85951	Homo sapiens exportin t mRNA complete cds
5807	2.1	X55740	Hs.76856	5' nucleotidase (CD73)
19747	2.1	H53572	Hs.32407	ESTs
38155	2.1	AA486777	Hs.105698	ESTs
924	2.1	G1112-HT1112	EST - HG1112-HT1112	
9544	2.1	H72630	Hs.35982	ESTs
8384	2.1	AA424282	Hs.91728	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds
25165	2.1	AA027837	Hs.30705	Retinitis pigmentosa 3 (X-linked recessive)
24348	2.1	W86469	Hs.77899	Tropomyosin alpha chain (skeletal muscle)
41401	2.1	R43334	Hs.55075	Homo sapiens KIAA0410 mRNA complete cds
35340	2.1	AA398900	EST - FIC_AA398900	
10898	2.1	AA112063	Hs.15313	ESTs Weakly similar to PRE-MRNA SPlicing HELICASE BRRI2 [S.cerevisiae]
381	2.1	D28473	Hs.78770	Isoleucine-tRNA synthetase

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22051	2.1	R49047	Hs.31975	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
3293	2.1	M94893	Hs.2051	Testis specific protein Y-linked
11528	2.1	AA236018	Hs.10724	ESTs Weakly similar to unknown [S.cervisiae]
11890	2.1	AA278323	Hs.17481	Homo sapiens clone 24606 mRNA sequence
13643	2.1	AA458578	Hs.12017	Homo sapiens clone 24477 mRNA sequence
19927	2.1	H71829	Hs.35701	ESTs
36511	2.1	AA429632	Hs.121018	ESTs
2130	2.1	L40407	Hs.9731	Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds
7193	2.1	AA046768	Hs.49476	Homo sapiens clone TUAS Cri-du-chat region mRNA
5448	2.1	X02751	Hs.69855	Neuroblastoma RAS viral (v-ras) oncogene homolog
35956	2.1	AA412533	Hs.109571	ESTs
7525	2.1	AA149259	Hs.69851	ESTs
39592	2.1	F09351	Hs.16492	ESTs Weakly similar to weakly similar to S. cerevisiae PTM1 precursor [C.elegans]
28029	2.1	AA478479	Hs.71992	ESTs
18425	2.1	AA232103	Hs.59112	ESTs
23494	2.1	T70045	Hs.16987	ESTs Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN F26A3.7 IN CHROMOSOME I [C.elegans]
				EST
30882	2.1	N56906	Hs.47996	Human TFIID subunit TAFI155 (TAFI155) mRNA complete cds
32597	2.1	T47333	Hs.77298	
33368	2.1	W80814	Hs.47283	ESTs
10259	2.1	R77527	Hs.29645	ESTs
21882	2.1	R43365	Hs.22273	ESTs
20590	2.1	N58146	Hs.34227	ESTs
12907	2.1	AA427577	Hs.26502	ESTs

**FIG.-3Cw**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22958	2.1	T10264	Hs.116122	ESTs
42044	2.1	T58753	Hs.24083	ESTs
4210	2.1	U31814	Hs.3352	Human transcriptional regulator homolog RPD3 mRNA complete cds
39	2.1	AB003698	Hs.28853	Homo sapiens mRNA for Cdc7-related kinase complete cds
14350	2.1	AA598831	Hs.17121	ESTs
29840	2.1	N21680	Hs.43047	ESTs
25593	2.1	AA113149	Hs.8130	Homo sapiens IPL (IPL) mRNA complete cds
26071	2.1	AA236880	Hs.118970	Protein phosphatase 2A regulatory subunit B' alpha-1
26529	2.1	AA278594	Hs.88461	EST
12154	2.1	AA291293	Hs.25219	ESTs
18817	2.1	F10077	Hs.12895	ESTs
6635	2.1	X99585	Hs.90182	H.sapiens mRNA for SMT3B protein
6681	2.1	Y00971	Hs.2910	Phosphoribosyl pyrophosphate synthetase 2
22077	2.1	R49482	Hs.5637	ESTs
11752	2.1	AA256042	Hs.24908	ESTs
41257	2.1	R31680	Hs.140902	ESTs
6904	2.1	Z34897	Hs.1570	Histamine receptor H1
16879	2.1	AA056538	Hs.63314	ESTs
38040	2.1	AA481403	Hs.107213	ESTs
4111	2.1	U26312	Hs.83550	Human heterochromatin protein HP1Hs-gamma mRNA complete cds
32878	2.1	W37448	Hs.41241	ESTs
21743	2.1	R40576	Hs.21590	ESTs Moderately similar to !!! ALU SUBFAMILY SX WARNING
25968	2.1	AA234935	ENTRY !!! [H.sapiens]	ESTs
			Hs.65032	ESTs

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24659	2.1	Z39211	Hs.12299	Homo sapiens GDP-L-fucose pyrophosphorylase (GFP)
38030	2.1	AA481148	Hs.105157	mRNA complete cds
61	2.0	AC002115	Hs.83379	ESTs
6306	2.0	X81625	Hs.77324	Cytochrome c oxidase subunit VIb
				EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR
				SUBUNIT 1
8203	2.0	AA382517	EST - AA382517	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10
34357	2.0	AA251430	Hs.5850	[Canis familiaris]
36972	2.0	AA442767	Hs.5049	Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase
28156	2.0	AA489057	Hs.8217	activation protein beta polypeptide
24434	2.0	W92787	Hs.17242	H.sapiens mRNA for nuclear protein SA-2
33508	2.0	W88772	Hs.50546	ESTs
				Human DNA sequence from cosmid F0811 on chromosome 6. Contains Daxx BING1 Tapasin RGL2 KE2 BING4 BING5 ESTs and CpG islands
37681	2.0	AA460675	Hs.31748	H.sapiens mRNA for TRE5
27125	2.0	AA405505	Hs.48295	Homo sapiens mRNA for putative RNA helicase 3' end
3780	2.0	U09851	Hs.112180	Zinc finger protein 148 (pHZ-52)
9112	2.0	D16611	Hs.89866	Coproporphyrinogen oxidase (coproporphyrin hydroxylase)
8357	2.0	AA418921	Hs.10325	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]
9133	2.0	D30946	Hs.28691	ESTs Highly similar to TRANSLOCON-ASSOCIATED
7519	2.0	AA147425	PROTEIN GAMMA SUBUNIT [Rattus norvegicus]	
14701	2.0	D59324	EST - AA147425_s	
380	2.0	D28423	ESTs	
				EST - D28423

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30571 825	2.0 2.0	N49595 D87328	Hs.46637 Hs.79375	ESTs Holocarboxylase synthetase (biotin-[propionyl-Coenzyme A-carboxylase (ATP-hydrolysing)]-ligase)
27744	2.0	AA452818	Hs.87385	ESTs Weakly similar to HYPOTHETICAL PROTEIN HI0034 [Haemophilus influenzae]
3997	2.0	U19906	Hs.2131	Arginine vasopressin receptor 1 (AVPR1)
22717	2.0	R91394	EST - FC_R91394	
377	2.0	D28364	EST - D28364	
28581 11790	2.0 2.0	C21163 AA256678	Hs.68608 Hs.17035	ESTs ESTs Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]
37931	2.0	AA478523	Hs.113613	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]
24678	2.0	Z39349	Hs.19575	ESTs Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]
10940	2.0	AA122217	Hs.19845	ESTs Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME II [C.elegans]
13964 15665 28379 13349	2.0 2.0 2.0 2.0	AA479048 W67631 AA609710 AA449269	Hs.142620 Hs.12342 Hs.42582 Hs.21198	ESTs Homo sapiens clone 24538 mRNA sequence ESTs ESTs Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa] ESTs Weakly similar to The KIAA0138 gene product is novel.
7322	2.0	AA090692	Hs.135552	[H.sapiens] EST - FC_H70641 ESTs
29358 24230	2.0 2.0	H70641 W722276	Hs.5950	

FIG.-3CZ

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
			CLUSTER	
40212	2.0	H88535	Hs.9564	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence
729	2.0	D83778	Hs.77698	Human mRNA for KIAA0194 gene partial cds
17951	2.0	AA165526	Hs.3833	Homo sapiens bifunctional ATP sulfurylase/adenosine 5'-phosphosulfate kinase mRNA complete cds
33943	2.0	AA171739	Hs.101590	ESTs
5870	2.0	X59244	Hs.74107	Zinc finger protein 43 (HTF6)
36319	2.0	AA425107	Hs.97016	ESTs
25654	2.0	AA126951	Hs.110857	ESTs Weakly similar to DNA-directed RNA polymerase [D.melanogaster]
16344	2.0	AA018907	Hs.5427	ESTs
8118	2.0	AA328993	Hs.104558	ESTs
29962	2.0	N25228	Hs.27349	ESTs
32236	2.0	R49327	Hs.57435	Natural resistance-associated macrophage protein 2
3279	2.0	M94065	Hs.94925	DIHYDROORotate DEHYDROGENASE PRECURSOR
16255	2.0	AA013349	Hs.60602	ESTs
37972	2.0	AA479215		EST - FIC_AA479215
41256	2.0	R31577	Hs.30696	ESTs
34834	2.0	AA292655	Hs.96557	ESTs
23169	2.0	T33215	Hs.112023	ESTs
29851	2.0	N22145	Hs.43094	ESTs
32862	2.0	W32519	Hs.55510	EST

FIG.\_3Da

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33616	>10	W93726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'5'-oligoisoadenylate synthetase-dependent inhibitor)
39995	>10	H62474	Hs.108240	EST
19328	>10	H17808	Hs.22858	ESTs
38590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
6106	>10	X70683	Hs.83484	SRY (sex determining region Y)-box 4
8648	>10	AA465016	Hs.69423	Homo sapiens serine protease-like protease (nes1) mRNA complete cds
5619	>10	X14850	Hs.2711	HISTONE H2A.X
5603	>10	X14253	Hs.75561	Teratocarcinoma-derived growth factor 1
37677	>10	AA460530	Hs.98384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
11561	>10	AA236533	Hs.19222	Evi-1
16490	>10	AA026418	Hs.91539	ESTs
32240	>10	R50976	Hs.12013	Ribonuclease L (2'5'-oligoisoadenylate synthetase-dependent inhibitor)
12480	>10	AA403116	Hs.9880	Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA complete cds
2114	>10	L41349	Hs.74014	Phospholipase C beta 4

**F/G..4Aa**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12143	>10	AA290991	Hs.17296	ESTs
33006	>10	W46286	Hs.107039	ESTs Weakly similar to ZK1058.5 [C.elegans]
39535	>10	F02450	Hs.111980	ESTs Moderately similar to unknown protein [H.sapiens]
6449	>10	X89986	Hs.32936	H.sapiens mRNA for NBK apoptotic inducer protein
37653	>10	AA460017	Hs.99513	ESTs
4178	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
				TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
1863	>10	L19161	Hs.121541	ESTs
19787	>10	H56679	Hs.37362	ESTs
8092	>10	AA316272	Hs.24550	ESTs
10747	>10	AA055841	Hs.31953	ESTs
5002	>10	U72761	Hs.6990	Human karyopherin beta 3 mRNA complete cds
33791	>10	Z40883	Hs.65588	ESTs
6188	>10	X76029	Hs.2841	NEURONMEDIN U-25 PRECURSOR
13136	>10	AA436560	Hs.7327	ESTs
5963	>10	X63629	Hs.2877	Cadherin 3 (P-cadherin)
38179	>10	AA487492	Hs.76272	Homo sapiens clone 23592 mRNA sequence
30938	>10	N58561	Hs.84898	Cathepsin B
17987	>10	AA169379	Hs.72865	ESTs
36695	>10	AA433910	Hs.98786	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE
10233	>10	R71427	Hs.9081	ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]
				ESTs
38330	>10	AA490882	Hs.112227	ESTs
1349	>10	HG4747-HT5195	HST - HG4747-HT5195	ESTs
36962	>10	AA442082	Hs.131915	ESTs
5510	>10	X05360	HS.58393	Cell division cycle 2 G1 to S and G2 to M
3021	>10	M68941	Hs.73826	Protein tyrosine phosphatase non-receptor type 4

**FIG.-4Ab**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17734	>10	AA137246	Hs.84980	ESTs
36371	>10	AA426017	Hs.109761	ESTs
459	>10	D38293	Hs.77770	Human mRNA for clathrin-like protein complete cds
17419	>10	AA113349	Hs.69588	EST
14054	>10	AA485223	Hs.34892	ESTs
5021	>10	U73524	Hs.87465	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds
4994	>10	U72514	Hs.12045	Human C2f mRNA complete cds
26355	>10	AA256379	Hs.99291	ESTs
4455	>10	U43944	Hs.14732	MALAT1 OXIDOREDUCTASE
10748	>10	AA055892	Hs.14543	ESTs
8111	>10	AA323787	Hs.4770	ESTs
19389	>10	H20165	Hs.31734	EST
32195	>10	R43471	Hs.22355	ESTs Weakly similar to ORF YOR258w [S.cerevisiae]
21519	>10	R27975	EST - FIC_R27975	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent)
6167	>10	X74987	Hs.12013	Ribonuclelease L (2'5'-oligoadenylate synthetase-dependent) inhibitor
41107	>10	R01634	Hs.119878	ESTs
5986	>10	X64810	Hs.78977	Proprotein convertase subtilisin/kexin type 1
11603	>10	AA243052	Hs.16389	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]
4702	>10	U57341	EST - U57341	
18676	>10	F04022	Hs.27885	ESTs
24197	>10	W67277	Hs.17546	ESTs
4713	>10	U57721	Hs.81771	Human L-kynurenine hydrolase mRNA complete cds
38460	>10	AA504462	Hs.105730	ESTs
18330	>10	AA216722	Hs.54481	Human mRNA for apolipoprotein E receptor 2 complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR	
18782	>10	F09739	Hs.12562	ESTs	
42766	>10	Z99394	Hs.94432	ESTs Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY' !!! [H.sapiens]	
34014	>10	AA191348	Hs.96178	ESTs	
16835	>10	AA054438	Hs.60753	ESTs	
29893	>10	N23003	Hs.42186	ESTs	
11160	>10	AA164289	Hs.26006	ESTs	
1158	>10	HG3344-HT3521		EST - HG3344-HT3521	
11813	>10	AA258158	Hs.22153	ESTs	
10992	>10	AA132523	Hs.22900	Homo :sapiens BAC clone RG1119C02 from 7p15	
5789	>10	X54925	Hs.83169	Matrix metalloproteinase 1 (interstitial collagenase)	
16993	>10	AA065300	Hs.75337	Human mRNA for KIAA0035 gene partial cds	
17654	>10	AA133250	Hs.62180	ESTs	
39436	>10	D52692	Hs.74574	Human Ca2+-dependent activator protein for secretion mRNA complete cds	
19727	>10	Hs.36690	ESTs		
41381	>10	R42278	Hs.31748	H.sapiens mRNA for TRE5	
22576	>10	R79111	Hs.29388	ESTs	
35769	>10	AA406206	Hs.104746	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	
33980	>10	AA180223	Hs.8454		
37084	>10	AA446486	Hs.125129	Homo :sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds	
26935	>10	AA347193	Hs.77831	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]	
2188	>10	L47276		EST - L47276	
4362	>10	U39817	Hs.36820	Bloom syndrome	

**FIG.\_4Ad**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9127	>10	D30037	Hs.91447	PHOSPHATIDYLINOSITOL
20614	>10	N59230	Hs.18937	ESTs
5692	>10	X17644	Hs.2707	G1 to S phase transition 1
4388	>10	U40714	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds
3598	>10	U01157	Hs.165	Glucagon-like peptide-1 receptor
24545	>10	Z38462	Hs.12403	ESTs
37456	>10	AA454632	Hs.123157	ESTs
10840	>10	AA084104	Hs.30177	ESTs
25179	>10	AA031268	Hs.113319	H.sapiens mRNA for kinesin-2
21	>10	AB000905	Hs.143080	H.sapiens histone H4 gene
18762	>10	F09458	Hs.12421	ESTs
39232	>10	AA621409	Hs.112986	ESTs
42602	>10	W86423	Hs.105413	ESTs
22372	>10	R62831	Hs.28366	EST
39110	>10	AA620709	Hs.20563	ESTs Weakly similar to HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II [C.elegans]
16810	>10	AA053636	Hs.129849	ESTs
29645	>10	H95840	Hs.42116	ESTs
36405	>10	AA426406	Hs.10801	Homo sapiens mRNA for KIAA0530 protein partial cds
4029	>10	U21090	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15006	>10	U30246	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
40594	>10	N35388	Hs.112227	ESTs
31484	>10	N69466	Hs.49683	ESTs
38601	>10	AA598738	Hs.109041	ESTs
40631	>10	N45124	Hs.6809	ESTs

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
236	>10	D13645	Hs.2471	Human mRNA for KIAA0020 gene complete cds
35803	>10	AA410295	Hs.97911	ESTs
19591	>10	H40688	Hs.33785	ESTs
38828	>10	AA609177	Hs.109363	ESTs
35798	>10	AA410231	Hs.98069	ESTs
3163	>10	M84424	Hs.1355	Cathepsin E
22400	>10	R64109	Hs.28487	ESTs
39062	>10	AA620333	Hs.112857	EST
25082	>10	AA017257	Hs.101139	ESTs
5857	>10	X58377	Hs.1721	Human mRNA for adipogenesis inhibitory factor
5214	>10	U83303	Hs.123029	H.sapiens mRNA for granulocyte chemotactic protein
36958	>10	AA442060	Hs.87507	ESTs
40660	>10	N49104	Hs.79108	NUCLEAR FACTOR RIP140
25951	>10	AA234556	Hs.135158	EST
22072	>10	R49406	Hs.28410	ESTs
39832	>10	H26279		EST - FIC_H26279
23198	>10	T40530	Hs.8241	ESTs Weakly similar to B0035.14 [C.elegans]
29331	>10	H68116	Hs.39063	ESTs
38316	>10	AA490500	Hs.18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
37829	>10	AA470084	Hs.98358	ESTs
3870	>10	U14518	Hs.1594	Centromere protein A (17kD)
39176	>10	AA621091	Hs.72087	ESTs
41793	>10	T03887	Hs.7327	ESTs
32277	>10	R61493	Hs.26886	Human mRNA for rod photoreceptor protein complete cds
5558	>10	X07876	Hs.89791	Wingless-type MMTV integration site 2 human homolog
6382	>10	X85133	Hs.85273	H.sapiens RBQ-1 mRNA

**F/G.\_4Af**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
			UNIGENE CLUSTER	
41040	>10	N91948	Hs.125034	ESTs
39080	>10	AA620552	EST - RC_AA620552_r	
20307	>10	N34830	Hs.37636	ESTs
18260	>10	AA206801	Hs.86277	ESTs
41065	>10	N93618	Hs.28554	ESTs
33109	>10	W59961	Hs.22564	Human mRNA for KIAA0389 gene complete cds
28015	>10	AA477421	Hs.21801	ESTs
30610	>10	N50138	Hs.47032	EST
34015	>10	AA191353	Hs.109884	ESTs
40559	>10	N33024	Hs.23450	ESTs
1445	>10	J03027	Hs.73885	MHC class I protein HLA-G
13242	>10	AA445994	Hs.21331	ESTs
37983	>10	AA479348	Hs.52871	H.sapiens mRNA for SYT
42242	>10	T89579	Hs.79353	Homo sapiens E2F-related transcription factor (DP-1)
				mRNA complete cds
37135	>10	AA447540	Hs.99112	EST
20564	>10	N55443	Hs.23625	ESTs
28141	>10	AA488432	Hs.56407	ESTs
21240	>10	R08613	Hs.20188	ESTs
34382	>10	AA252512	Hs.100069	ESTs
25948	>10	AA234365	Hs.102456	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds
40913	>10	N69218	Hs.108232	ESTs
35697	>10	AA405512	Hs.104741	ESTs
34672	>10	AA284372	Hs.111471	ESTs
3659	>10	U04313	Hs.55279	Protease inhibitor 5. (maspin)
17051	>10	AA070801	Hs.51615	ESTs

**FIG.-4Ag**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19203 20791	>10 >10	H11593 N68057	Hs.28116- Hs.90357	ESTs Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
24215 37246	>10 >10	W69425 AA449311	Hs.15767 Hs.98658	ESTs Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds
6790	>10	Y12394	Hs.3886	Homo sapiens importin-alpha homolog (SRP19gamma) mRNA complete cds
25806 36307	>10 >10	AA149007 AA424803	Hs.103871 Hs.98474	EST EST
25047	>10	AA011031	Hs.110182	ESTs
33343	>10	W79834	HS.58559	ESTs Weakly similar to rhodokin [M.musculus]
5799	>10	X55330	Hs.111661	Aspartylglucosaminidase
23623	>10	T84047	Hs.15428	ESTs
29523	>10	H88353	Hs.139312	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]
26291	>10	AA253422	Hs.142179	ESTs
35801	>10	AA410291	Hs.114121	ESTs
40064	>10	H72283	Hs.38483	Human mRNA for KIAA0265 gene partial cds
29795	>10	N20641	Hs.46230	ESTs Highly similar to HYPOTHETICAL MYELOID CELL-LINE PROTEIN 3 [Homo sapiens]
5960	>10	X63575	Hs.89512	ATPase: Ca++ transporting plasma membrane 2 (NOTE: redefinition of symbol)
37611	>10	AA458996	Hs.32970	Human signaling lymphocytic activation molecule (SLAM) mRNA complete cds
26274 37168 39433	>10 >10 >10	AA253011 AA447772 D52037	Hs.88756 Hs.125153 Hs.35650	ESTs ESTs Human thymidine kinase 2 (TK2) mRNA complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER		UNIGENE DESCRIPTOR
			UNIGENE	CLUSTER	
1570	>10	K01383			EST - K01383
30617	>10	N50646	Hs.47083	ESTs	
35106	>10	AA371561	Hs.142355	ESTs	Weakly similar to putative p150 [H.sapiens]
789	>10	D86971	Hs.78851	ESTs	Human mRNA for KIAA0217 gene partial cds
4386	>10	U40622	Hs.21523	ESTs	DNA repair protein XRCC4
31944	>10	N93193	Hs.80310	ESTs	
13237	>10	AA443971	Hs.142495	ESTs	Weakly similar to !!! ALU SUBFAMILY J WARNING
4157	>10	U28811	Hs.78979	ESTs	ENTRY !!! [H.sapiens]
					Human cysteine-rich fibroblast growth factor receptor (CFR-1)
2123	>10	L40396	Hs.26956	ESTs	mRNA complete cds
26926	>10	AA342402	Hs.48729	ESTs	Homo sapiens (clone s22i71) mRNA fragment
6479	>10	X91653			
11969	>10	AA280670	Hs.24968	ESTs	
37601	>10	AA458864	Hs.102946	ESTs	
28644	>10	D12163	Hs.103262	ESTs	
40604	>10	N38893	Hs.28578	ESTs	Homo sapiens KIAA0428 mRNA complete cds
3913	>10	U16261	Hs.66576	ESTs	Human MDA-7 (mda-7) mRNA complete cds
23759	>10	T90313	Hs.16732	ESTs	
2857	>10	M58597	Hs.2173	ESTs	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)
34518	>10	AA278721	Hs.103104	ESTs	
18008	>10	AA171895	Hs.30057	ESTs	Homo sapiens clone 24749 and 24750 mRNA sequences
19001	>10	H02890	Hs.29885	ESTs	
39488	>10	D60831	Hs.126021	ESTs	
23360	>10	T58531	Hs.141905	ESTs	
34105	>10	AA207123	Hs.130857	ESTs	

FIG.-4*A*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38121	>10	AA485724		EST - RC_AA485724
29080	>10	FI3655	Hs.65638	ESTs Moderately similar to !!! ALU SUBFAMILY SB1 WARNING ENTRY !!! [H.sapiens]
9723	>10	L44542	Hs.126923	ESTs
25215	>10	AA035540	Hs.1255	APOLIPOPROTEIN AI REGULATORY PROTEIN-1
39218	>10	AA621330	Hs.114381	ESTs
20088	>10	N20054	Hs.20325	ESTs Weakly similar to putative p150 [H.sapiens]
33713	>10	Z39427	Hs.65748	ESTs
18392	>10	AA227751	Hs.55896	ESTs
42390	>10	W40150	Hs.24485	Homo sapiens chromosome-associated polypeptide (HCAP) mRNA complete cds
35693	>10	AA405485	Hs.96854	ESTs Weakly similar to similar to t complex testis-specific protein [C.elegans]
35500	>10	AA400715	Hs.107479	ESTs
1856	>10	L18920	Hs.36980	MELANOMA-ASSOCIATED ANTIGEN 2
36258	>10	AA423962	Hs.108465	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
37068	>10	AA446312	Hs.22143	ESTs Weakly similar to !!! ALU CLASS C WARNING ENTRY!!! [H.sapiens]
33020	>10	W46891	Hs.55968	ESTs Weakly similar to polypeptide N-acetylgalactosaminyltransferase [H.sapiens]
27037	>10	AA400198	Hs.93753	ESTs
40827	>10	N64051	Hs.48920	Homo sapiens Werner syndrome gene complete cds
3375	>10	S50223	Hs.108642	HKR- <sup>r1</sup>
37310	>10	AA451707	Hs.99246	ESTs
38235	>10	AA489030	Hs.105223	ESTs
22258	>10	R56432	Hs.26536	ESTs

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
	ACCESSION		
36845	>10	AA436198	Hs.103902 ESTs
28323	>10	AA599639	Hs.50216 ESTs
30207	>10	N33920	Hs.44532 H.sapiens mRNA for diubiquitin
6494	>10	X92689	Hs.55823 H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
36288	>10	AA424502	Hs.98402 ESTs
37546	>10	AA456641	Hs.99433 ESTs
4193	>10	U31116	Human beta-sarcoglycan A3b mRNA complete cds
37777	>10	AA464860	Homo sapiens Jak2 kinase mRNA complete cds
38280	>10	AA489791	EST - RC_AA489791
2343	>10	M15353	Eukaryotic translation initiation factor 4E
39045	>10	AA610077	Hs.79306 Hs.102314 ESTs
35495	>10	AA400527	Hs.111914 ESTs
3522	>10	S80267	Hs.74101 Spleen tyrosine kinase
22282	>10	R55197	Hs.21320 ESTs
32740	>10	T92950	Hs.91077 ESTs
37057	>10	AA446131	Hs.124918 ESTs
34107	>10	AA209469	Hs.96297 ESTs
34391	>10	AA252703	EST - RC_AA252703
33301	>10	W73883	Hs.58174 ESTs
765	>10	D86096	Prostaglandin E receptor 3 (subtype EP3) {alternative products}
7785	>10	AA243375	Hs.495 EST - AA243375
34070	>10	AA196549	Hs.6592 ESTs
6041	>10	X67155	Hs.75530 MITOTIC KINESIN-LIKE PROTEIN-1
33890	>10	HUMTFRR/M11507	AFFX-HUMTFRR/M11507_5
35277	>10	AA398536	Hs.97365 ESTs
26059	>10	AA236685	Hs.58940 ESTs

**FIG.\_4Ak**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
	ACCESSION		
25801	>10	AA148530	EST - RC_AA148530
32258	>10	R55623	ESTs
34554	>10	AA280016	DNA polymerase gamma
32034	>10	N98926	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]
4787	>10	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds
1684	>10	L07541	Replication factor C (activator 1) 3 (38kD)
18718	>10	F04915	ESTs
40427	>10	N21147	ESTs
32635	>10	T61116	ESTs
4306	>10	U36798	Homo sapiens platelet cG1-PDE mRNA complete cds
38211	>10	AA488687	ESTs
6438	>10	X89398	URACIL-DNA GLYCOSYLASE 1 PRECURSOR
38580	>10	AA598545	ESTs
4945	>10	U69108	Homo sapiens mRNA for TRAF5 complete cds
41654	>10	R76437	THROMBOXANE-A SYNTHASE
41163	>10	R08176	ESTs
34400	>10	AA253400	ESTs
35822	>10	AA411144	ESTs
26628	>10	AA280641	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]
40204	>10	H88296	EST - RC_H88296
19164	>10	H10395	EST
26240	>10	AA252282	Human mRNA for KIAA0152 gene complete cds
8963	>10	HUMTFR/M11507	AFFX-HUMTFR/M11507_M
35322	>10	AA398710	H. sapiens RNA for CLCN3
1210	>10	HG37-HT37	EST - HG37-HT37

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22793	>10	R96208	Hs.35533	ESTs
36052	>10	AA417027	Hs.104787	EST
26574	>10	AA279504	Hs.88629	ESTs
35197	>10	AA398120	Hs.97504	ESTs
37979	>10	AA479295	Hs.106290	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melalogaster]
4862	>10	U65437	Hs.95838	Human homeodomain-containing protein (HANF) mRNA complete cds
26700	>10	AA282197	Hs.89002	EST
35049	>10	AA350857	Hs.22507	ESTs
40083	>10	H73466	Hs.79086	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3
17541	>10	AA127459	Hs.108788	ESTs
19949	>10	H78263	Hs.124151	ESTs
4477	>10	U45880	Hs.37137	Human IAP-like protein ILP mRNA complete cds
26916	>10	AA331393	Hs.47378	ESTs
34188	>10	AA228030	Hs.120234	ESTs
29229	>10	H48459	Hs.36232	Human mRNA for KIAA0186 gene complete cds
42773	>10	YEL019c/MMS21	EST - YEL019c/MMS21	
32189	>10	R43183	Hs.95044	ESTs
36739	>10	AA435610	EST - RC_AA435610	
31310	>10	N66891	Hs.49268	EST
26545	>10	AA278979	Hs.88547	ESTs
21902	>10	R43822	Hs.22691	EST
25925	>10	AA164494	Hs.29417	ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H.sapiens]
29344	>10	H68839	Hs.38782	EST
1346	>10	HG4716-HT5158	EST - HG4716-HT5158	

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
		ACCESSION	
218	>10	D13540	PROTEIN-TYROSINE PHOSPHATASE 2C
26100	>10	AA242835	Hs.5917 Human mRNA for KIAA0391 gene complete cds
41593	>10	R64129	ESTs
42290	>10	T95105	ESTs
6713	>10	Y08564	EST Y08564
33377	>10	W81219	ESTs Weakly similar to F46B6.7 [C.elegans]
31619	>10	N73449	ESTs
26718	10.0	AA282576	ESTs
21558	10.0	R33112	Human AF-6 mRNA complete cds
40113	10.0	H78003	ESTs
10801	10.0	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C.elegans]
37491	10.0	AA455239	ESTs Highly similar to CHROMOSOME CONDENSATION DPY-27 [Caenorhabditis elegans]
254	9.9	D14657	ESTs Human mRNA for KIAA0101 gene complete cds
29693	9.9	H97819	ESTs
26525	9.8	AA278392	ESTs
13110	9.8	AA435840	Hom sapiens mRNA for high mobility group protein HMG2a
34863	9.7	AA299784	EST
39432	9.7	D51691	Phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosylaminoimidazole synthetase
31572	9.6	N71294	ESTs
17903	9.6	AA160259	EST
20747	9.6	N66842	ESTs
4676	9.6	U55206	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds

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**FIG.\_4An**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34363	9.6	AA251587	Hs.10801	Homo sapiens mRNA for KIAA0530 protein partial cds
39094	9.5	AA620636	Hs.112264	ESTs
3888	9.5	U15128	Hs.36573	Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
39386	9.5	D12184	Hs.3350	ESTs
4192	9.4	U31099	Hs.121479	Human DP prostanoïd receptor (PTGDR) mRNA partial cds
4507	9.4	U47050	Hs.24852	Human putative calcium influx channel (htrp3) mRNA complete cds
35606	9.4	AA402227	Hs.97345	ESTs Moderately similar to N-tropomodulin [R.norvegicus]
19829	9.3	H58813	Hs.37629	EST
14837	9.3	T40145	Hs.21921	ESTs
17336	9.3	AA099585	Hs.41175	ESTs
29496	9.2	H85434	Hs.40672	EST
29943	9.2	N24786	Hs.42993	ESTs Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
17997	9.2	AA169633	Hs.72835	EST
13883	9.1	AA476917	Hs.34627	ESTs Weakly similar to No definition line found [C.elegans]
30539	9.1	N49072	Hs.93968	ESTs
26380	9.1	AA257012	Hs.88054	EST
40812	9.0	N63419	Hs.83389	ESTs
903	9.0	D90070	Hs.96	ATL-derived PMA-responsive (APR) peptide
22674	9.0	R87160	Hs.33665	ESTs
15244	8.9	W00904	Hs.8037	ESTs
18269	8.9	AA209467	Hs.92489	ESTs
19662	8.9	H47391	Hs.33947	ESTs
2548	8.8	M25897	Hs.81564	Platelat factor 4
7736	8.8	AA232121	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
	ACCESSION		
39939	8.8	H53454	EST - RC_H53454
25111	8.7	AA020787	ESTs
21655	8.7	R38239	EST
27074	8.6	AA401475	ESTs Weakly similar to C36B1.3 [C.elegans]
4959	8.5	U70322	ESTs.39733 Human transportin (TRN) mRNA complete cds
2315	8.5	M14123	EST - M14123_xpt1
37253	8.5	AA449357	ESTs
39624	8.5	F10836	ESTs
23213	8.5	T40891	ESTs
2798	8.5	M54995	Connactive tissue activation peptide III
32479	8.4	T16282	WEE'-LIKE PROTEIN KINASE
19081	8.4	H06701	ESTs Weakly similar to RHOMBOTIN-1 [H.sapiens]
21098	8.3	R00545	ESTs
14723	8.3	D59894	ESTs
37154	8.3	AA447666	Human CENP-F kinetochore protein mRNA complete cds
8068	8.3	AA313387	ESTs Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK10;8.1 IN CHROMOSOME III [Caenorhabditis elegans]
7485	8.3	AA129547	ESTs
16501	8.3	AA026969	ESTs
34527	8.2	AA279091	ESTs
6700	8.2	Y07867	H.sapiens mRNA for Pirin isolate 1
2852	8.2	M58460	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds
11188	8.2	AA172372	ESTs
42293	8.2	T95333	ESTs Weakly similar to coded for by C. elegans cDNA yk110;8.3 [C.elegans]
5443	8.2	X02530	Interferon (gamma)-induced cell line protein 10 from EST - RC_T59505
23371	8.1	T59505	

FIG.-4Ap

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17306	8.1	AA086201	Hs.92702	ESTs
18497	8.1	AA233795	Hs.65828	ESTs
235	8.1	D13644	Hs.140933	Human mRNA for KIAA0019 gene complete cds
24525	8.1	Z38347	Hs.118338	ESTs
7826	8.1	AA248884	EST .. AA248884	
32142	8.1	R38715	Hs.123918	Homo sapiens clone 24540 mRNA sequence
39067	8.1	AA620405	Hs.112860	ESTs
6235	8.0	X78416	Hs.3155	Casein alpha S1
29517	8.0	H88261	Hs.41116	ESTs
39344	7.9	C21034	Hs.76822	ESTs Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]
18951	7.9	H00580	Hs.29889	ESTs
18953	7.9	H00615	Hs.24227	ESTs
18376	7.9	AA226925	Hs.88057	ESTs
36023	7.8	AA416881	Hs.97383	ESTs
2192	7.8	L48211	Hs.20954	Homc Sapiens angiotensin II receptor gene complete cds
33016	7.8	W46577	Hs.41716	H.sapiens mRNA for ESM-1 protein
40614	7.7	N39257	Hs.99291	ESTs
36295	7.7	AA424534	Hs.98415	ESTs
19564	7.7	H38833	Hs.32838	ESTs
16914	7.7	AA058665	Hs.23744	ESTs
35967	7.6	AA412694	Hs.6891	Human splicing factor SRp55-2 (SRp55) mRNA complete cds
21672	7.6	R38635	Hs.12328	ESTs
19918	7.6	H69787	Hs.14699	ESTs
17721	7.6	AA136590	Hs.71711	ESTs
26134	7.6	AA243763	Hs.87694	ESTs
18766	7.6	F09497	Hs.12755	ESTs

**FIG.-4Aq**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34492	7.5	AA262439	Hs.96	ATL-derived PMA-responsive (APR) peptide
270	7.5	D14822	EST · D14822	
35975	7.4	AA412738	Hs.3688	ESTs
29842	7.4	N21688	Hs.43050	ESTs
5793	7.4	X54942	Hs.83758	CDC28 protein kinase 2
31571	7.4	N71250	Hs.50004	ESTs
23765	7.4	T90443	Hs.15053	ESTs Weakly similar to KIAA0376 [H.sapiens]
35123	7.3	AA380927	Hs.97113	EST
38252	7.3	AA489247	Hs.105234	ESTs
38216	7.3	AA488861	Hs.134943	ESTs
29418	7.2	H77915	EST · RC_H77915	
42504	7.2	W699803	Hs.103159	ESTs
6111	7.2	X71125	Hs.79033	H.sapiens mRNA for glutamine cyclotransferase
41173	7.2	T03024	Hs.29170	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]
9951	7.1	N71513	Hs.39328	ESTs
28109	7.1	AA485212	Hs.9591	ESTs
988	7.1	HG2160-HT2230	EST - HG2160-HT2230	
29848	7.1	N22107	Hs.124215	ESTs
30628	7.1	N50744	Hs.124025	ESTs
22567	7.0	R77771	Hs.129445	ESTs
9347	7.0	H03686	Hs.112013	ESTs
11696	7.0	AA252894	Hs.20474	ESTs
40584	7.0	N34870	Hs.102520	EST
193	7.0	D10923	Hs.137555	PROEABLE G PROTEIN-COUPLED RECEPTOR HM174
18305	7.0	AA214048	Hs.259	Collagen type IV alpha 4
60778	7.0	X69141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
26741	6.9	AA283198	Hs.89113	ESTs

**FIG.\_4Ar**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
35069	6.9	AA358397	Hs.97007	EST
23504	6.9	T71042	Hs.12066	ESTs
299	6.9	D16815	Hs.37288	Homo sapiens orphan nuclear hormone receptor BD73 mRNA 3' end
40583	6.9	N34855	Hs.109099	ESTs
39524	6.9	F01905	Hs.14732	MALATE OXIDOREDUCTASE
34578	6.8	AA280837	Hs.111429	ESTs
9326	6.8	D89377	Hs.89404	Msh (Drosophila) homeo box homolog 2
19188	6.8	H11255	Hs.12887	ESTs Highly similar to ACTIN-LIKE PROTEIN [Bos taurus]
18185	6.8	AA194983	Hs.81791	Homo sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds
1566	6.7	J05614	EST - J05614	
25675	6.7	AA129757	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
5814	6.7	X56088	Hs.1644	CYTICHROME P450 VII
13861	6.6	AA470145	Hs.25130	ESTs
29794	6.6	N20598	Hs.94288	ESTs
39333	6.6	C20910	Cyclin B1	
3770	6.6	U09609	Hs.73090	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
31831	6.6	N89894	Hs.91454	ESTs
33063	6.6	W53000	Hs.56155	Homo sapiens clone 24431 mRNA sequence
20326	6.6	N35583	Hs.8768	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]
42596	6.5	W85900	Hs.109333	ESTs
39606	6.5	F10243	Hs.140873	ESTs Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14617	6.5	C14983	Hs.37380	ESTs
27360	6.4	AA425356	Hs.89306	ESTs
20126	6.4	N22015	Hs.18457	ESTs
6663	6.4	Y00291	Hs.82783	RETINOIC ACID RECEPTOR BETA-2
36472	6.4	AA428633	Hs.98604	EST
9578	6.4	H87652	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds
37308	6.4	AA451694	Hs.99244	EST
16101	6.4	AA002147	Hs.59952	EST
20629	6.3	N59798	Hs.18917	ESTs
36100	6.3	AA417740	Hs.96345	ESTs
32882	6.3	W37683	Hs.55080	ESTs
18072	6.3	AA180448	Hs.144300	EST
28125	6.3	AA486073	Hs.57362	ESTs
37464	6.2	AA454747	Hs.14934	ESTs
1441	6.2	J02963	Hs.785	Integrin alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex antigen-CD41B)
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal ESTs Weakly similar to tetracycline transporter-like protein [M.musculus]
32570	6.1	T30222	Hs.4220	
32504	6.1	T17063	Hs.65721	EST
10867	6.1	AA088458	Hs.19322	ENTFY !!! [H.sapiens]
14528	6.1	AA620295	Hs.99821	ESTs
29454	6.1	H81308	Hs.40253	EST
21940	6.0	R44538	Hs.140889	ESTs
29066	6.0	F10927	Hs.66163	Homo sapiens clone 23636 mRNA sequence
18062	6.0	AA179845	Hs.73625	ESTs Moderately similar to rabkinatin-6 [M.musculus]

**FIG.\_4At**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
ACCESSION			
41745	6.0	R95895	Hs.142677 ESTs
8787	6.0	AA504307	X-LINKED HELICASE II
693	5.9	D80007	Hs.96264 Human mRNA for KIAA0185 gene partial cds
4093	5.9	U25182	Hs.45028 Human antioxidant enzyme AOE37-2 mRNA complete cds
1192	5.9	HG3546-HT3744	EST - HG3546-HT3744
22956	5.9	T10248	ESTs
36723	5.9	AA435524	Hs.4280 ESTs
2114	5.9	L40384	EST - L40384
26872	5.9	AA291137	Hs.97483 ESTs
6602	5.9	X98266	EST - X98266_cds2
42701	5.9	Z38612	ESTs
28573	5.8	C21118	Hs.144000 ESTs
18290	5.8	AA211901	Hs.84541 ESTs
5330	5.8	U91327	Hs.86430 ESTs
2553	5.8	M26167	EST - U91327
			Human platelet factor 4 variation 1 (PF4var1) gene complete cds
38180	5.8	AA487495	EST - RC_AA487495
4244	5.7	U33286	Human chromosome segregation gene homolog CAS mRNA complete cds
3977	5.7	U18991	Hs.2133 Retinal pigment epithelium-specific protein (65kD)
24673	5.7	Z39301	Hs.7859 ESTs
6928	5.7	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
			ESTs
38726	5.7	AA608733	Hs.138663 Human mRNA for KIAA0029 gene partial cds
39290	5.7	C14573	Hs.75383 ESTs
11405	5.7	AA232231	Hs.24596 ESTs
6329	5.6	X822279	EST - X82279

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2545	5.6	M25753	Hs.23960	Cyclin B1
33592	5.6	W93127	Hs.59422	ESTs
28843	5.6	D60252	Hs.113619	ESTs
6160	5.6	X74794	Hs.89699	CDC21 HOMOLOG
42515	5.5	W72116	Hs.106333	Homo sapiens clone 23622 mRNA sequence
4732	5.5	U58522	Hs.84713	Human huntingtin interacting protein (HIP2) mRNA complete cds
3299	5.5	M95623	Hs.82609	Hydroxymethylbilane synthase
28320	5.5	AA599574	Hs.65370	ESTs
746	5.5	D84454	Hs.21899	Human mRNA for UDP-galactose translocator complete cds
31117	5.4	M81182	Hs.76781	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)
21257	5.4	R09196	Hs.20321	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]
31487	5.4	N69507	Hs.129849	ESTs
28954	5.4	F03153	Hs.90383	ESTs
38928	5.4	AA609595	Hs.109960	ESTs
29903	5.4	N23366	Hs.93664	EST
28209	5.3	AA491250	Hs.54990	ESTs
9470	5.3	H46617	EST - H46617	
9435	5.3	H30201	EST - H30201	
27411	5.3	AA428137	Hs.86434	ESTs
30615	5.3	N50556	Hs.47076	ESTs
29934	5.3	N24194	Hs.43531	ESTs
1094	5.2	HG2846-HT2983	EST - HG2846-HT2983	
11232	5.2	AA186804	Hs.25740	ESTs Weakly similar to unknown [S.cerevisiae]
26843	5.2	AA287450	Hs.93842	ESTs
8035	5.2	AA305116	EST - AA305116	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19263	5.1	H15054	Hs.22184	ESTs
24596	5.1	Z38810	Hs.27194	ESTs
28589	5.1	C21245	Hs.11171	H.sapiens mRNA for apoptosis specific protein
5684	5.1	X17098	Hs.108938	Pregnancy-specific beta-1 glycoprotein 6
30710	5.1	N51761	Hs.47338	EST
26360	5.1	AA256460	Hs.44610	ESTs
2351	5.1	M15796	Hs.78996	Proliferating cell nuclear antigen
30262	5.1	N35065	Hs.44690	Homo sapiens clone 24739 mRNA sequence
41792	5.1	T03886	Hs.100265	ESTs
36710	5.1	AA434411	Hs.98806	ESTs
42185	5.1	T79951	Hs.111805	ESTs
18745	5.0	F09134	Hs.12839	ESTs
35746	5.0	AA406063	Hs.98003	ESTs
36900	5.0	AA436866	Hs.86178	H.sapiens mRNA for M-phase phosphoprotein mpp9
27595	5.0	AA443328	Hs.12544	ESTs
27117	5.0	AA405098	Hs.38178	ESTs Weakly similar to MOESIN/EZFRIN/RADIXIN HOMOLOG [D.melanogaster]
33458	5.0	W86835	Hs.14158	Homo sapiens mRNA for KIAA0636 protein complete cds
26693	5.0	AA282120	Hs.88975	EST
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
29701	5.0	H97970	Hs.42476	EST
34828	4.9	AA292436	Hs.27621	Homo sapiens semaphorin F homolog mRNA complete cds
14985	4.9	U15128	Hs.36573	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds
34761	4.9	AA2877833	Hs.99668	ESTs
23211	4.9	T40889	Hs.8329	ESTs

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40611	4.9	N39138	Hs.106794	Homo sapiens mRNA for KIAA0584 protein partial cds
42611	4.9	W87006	Hs.79440	Homo sapiens putative RNA binding protein KOC (koc) mRNA complete cds
17581	4.9	AA129395	Hs.71139	EST
18712	4.9	F04677	Hs.12381	ESTs
30709	4.9	N51752	Hs.47334	ESTs Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]
34179	4.9	AA227903	Hs.4i127	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]
1285	4.8	HG4157-HT4427		EST · HG4157-HT4427
1106	4.8	HG2981-HT3127		EST · HG2981-HT3127
34367	4.8	AA251758	Hs.40323	Homo sapiens spleen.mitotic checkpoint BUB3 (BUB3) mRNA complete cds
34802	4.8	AA291468	Hs.98504	ESTs
11595	4.8	AA242819	Hs.32539	ESTs
8295	4.8	AA405082	Hs.125014	ESTs
17622	4.8	AA131584	Hs.71435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754	4.7	AA287642	Hs.81848	Human mRNA for KIAA0078 gene complete cds
37667	4.7	AA460318	Hs.110165	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]
38622	4.7	AA598967	Hs.141982	ESTs
25038	4.7	AA010065	Hs.83758	CDC28 protein kinase 2
32503	4.7	T17045	Hs.90283	Collagen type I alpha-2
3278	4.7	M94055	Hs.54499	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT
9696	4.7	L38961	Hs.89650	Integral transmembrane protein 1
36387	4.7	AA426270	Hs.98498	ESTs

FIG.-4Ax

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
31381 26723	4.7 4.7	N67889 AA282781	Hs.49397 Hs.95321	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]
30594 38286	4.6 4.6	N49967 AA489847	Hs.46624 Hs.112019	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]
14474	4.6	AA609427	Hs.24164	ESTs Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]
5312 35588 29739 7203 2157	4.6 4.6 4.6 4.6 4.6	U90716 AA401750 H99626 AA053096 L41939	Hs.79187 Hs.97343 Hs.42710	Human cell surface protein HCAR mRNA complete cds EST EST EST .. AA053096 Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
32086 8085	4.6 4.6	R11510 AA314779	Hs.52054 Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
224 33656 34065	4.6 4.6 4.6	D13633 W95477 AA195517	Hs.77695 Hs.50582 Hs.111160	Human mRNA for KIAA0008 gene complete cds ESTs ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
6028 4166 41069 8264 27588 35882	4.5 4.5 4.5 4.5 4.5 4.5	X66503 U29463 N93969 AA401334 AA443187 AA412047	Hs.90011 Hs.108102 Hs.91107 Hs.106941 Hs.41181 Hs.122578	Adenylosuccinate synthase Cytochrome B561 H.sapiens mRNA for hFat protein ESTs ESTs ESTs

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34479	4.5	AA262080	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKC21) mRNA complete cds
15921	4.5	Y12065	Hs.5092	Hom sapiens mRNA for nucleolar protein hNop56
11279	4.4	AA195399	Hs.24641	ESTs
39222	4.4	AA621348	Hs.110042	ESTs Highly similar to DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]
8771	4.4	AA491188	Hs.62273	ESTs
7898	4.4	AA263032	Hs.81634	ESTs
19902	4.4	H66736	Hs.34180	ESTs
10716	4.4	AA053319	Hs.9951	ESTs
13193	4.4	AA442763	Hs.20483	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
17983	4.4	AA169226	Hs.72782	ESTs
31680	4.3	N74438	Hs.50492	ESTs
28731	4.3	D20981	Hs.92453	EST
28348	4.3	AA608752	Hs.71969	ESTs
33036	4.3	W48580	Hs.39972	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]
28106	4.3	AA485084	Hs.110462	ESTs
38690	4.3	AA600121	Hs.111467	ESTs
20203	4.3	N26855	Hs.5858	ESTs Moderately similar to !!! ALU SUBFAMILY SQ WARNING
10251	4.3	R76185	Hs.18171	ENTFY !!! [H.sapiens]
31636	4.3	N73680	Hs.57435	ESTs Weakly similar to C01H6.7 [C.elegans]
1572	4.2	K01884	Natural resistance-associated macrophage protein 2	EST - K01884
10923	4.2	AA116036	Hs.9329	ESTs

**FIG.-4A2**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34380	4.2	AA252414	Hs.104300	ESTs
10132	4.2	R35733		EST - R35733
16629	4.2	AA036811	Hs.61859	ESTs
25146	4.2	AA026356	Hs.108106	ESTs
28730	4.2	D20959	Hs.5858	ESTs Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]
10200	4.2	R64521	Hs.77361	ESTs
38695	4.2	AA600176	Hs.112345	ESTs
31365	4.2	N67550	Hs.48907	ESTs
42379	4.1	W37999	Hs.103018	ESTs
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
26220	4.1	M29474	Hs.73958	Human recombination activating protein (RAG-1) gene complete cds
8927	4.1	AF008442	Hs.5409	Hom <sub>c</sub> sapiens RNA polymerase I subunit hRPA39 mRNA complete cds
13379	4.1	AA449741	Hs.4029	ESTs Weakly similar to AF-9 PROTEIN [H.sapiens]
5134	4.1	U79293	Hs.90802	Human clone 23948 mRNA sequence
36575	4.1	AA431085	Hs.98706	EST
143	4.1	HUMTFR/M11507	AFFX-HUMTFR/M11507_5	
10970	4.1	AA129390	Hs.5285	ESTs
25836	4.1	AA152305	Hs.2248	Interferon (gamma)-induced cell line protein 10 from
19735	4.1	H53038	Hs.36710	EST
40711	4.1	N53564	Hs.108159	ESTs
4149	4.1	U28386	Hs.2397	RAG (recombination activating gene) cohort 1
5767	4.1	X53793	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
5503	4.1	X05232	Hs.83326	Stromelysin

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20310	4.1	N34893	Hs.6153	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B028.J.9 IN CHROMOSOME III [Caenorhabditis elegans]
456	4.1	D38145	Hs.61333	ESTs Prostaglandin I2 (prostacyclin) synthase
33651	4.0	W95409	Hs.59704	ESTs
19110	4.0	H08778	Hs.133521	ESTs
24408	4.0	W90146	Hs.35962	ESTs
26596	4.0	AA279943	Hs.88671	ESTs
32969	4.0	W42451	Hs.92260	ESTs
27006	4.0	AA398695	Hs.56159	ESTs Weakly similar to E04F6.2 gene product [C.elegans]
29809	4.0	N21043	Hs.42932	EST
9596	3.9	H91564	Hs.13540	ESTs
29024	3.9	F09315	Hs.76982	Homo sapiens mRNA for KIAA0583 protein partial cds
21694	3.9	R39317	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2)
37865	3.9	AA476623	Hs.99819	mRNA complete cds ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe] AFFX-HUMTFR/M11507_3
8961	3.9	HUMTFR/M11507	Hs.6823	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
24862	3.9	Z41415	Hs.79656	ESTs
26685	3.9	AA281950	Hs.100703	ESTs
42300	3.9	T95850	Hs.3057	Zinc finger protein 74 (Coss52)
6495	3.9	X92715	Hs.111496	ESTs
38604	3.9	AA598803	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
30560	3.9	N49284	Hs.14366	ESTs
14413	3.9	AA600150	Hs.105703	EST
38158	3.9	AA487021		

**FIG.\_4Bb**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2572	3.9	M27281	Hs.73793	Vascular endothelial growth factor
40100	3.8	H75933	Hs.75901	Laminin receptor (2H5 epitope)
20944	3.8	N74443	Hs.16247	ESTs
8513	3.8	AA446990	Hs.103135	ESTs
13877	3.8	AA476604	Hs.7114	ESTs
14509	3.8	AA609943	Hs.32793	ESTs
10281	3.8	R80333	Hs.21182	ESTs
25284	3.8	AA045074	Hs.110146	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]
6730	3.8	Y09305	Hs.17154	H.sapiens mRNA for protein kinase Dyrk4 partial
16033	3.8	HUMISGF3A/M97935	AFFX-HUMISGF3A/M97935_MB	
39242	3.8	AA621523	Hs.110832	ESTs
27354	3.8	AA425221	Hs.81688	ESTs
4552	3.8	U49188	Hs.76329	Human placenta (Diff33) mRNA complete cds
18385	3.8	AA227219	Hs.110826	Homo sapiens CAGF9 mRNA partial cds
16754	3.8	AA046067	EST . RC_AA046067	
42463	3.8	W60180	Hs.103135	ESTs
867	3.7	D87716	Hs.90315	Human mRNA for KIAA0007 gene partial cds
31195	3.7	N80703	Hs.50473	ESTs
22828	3.7	R98192	Hs.35828	ESTs
25240	3.7	AA039713	Hs.110406	ESTs
4341	3.7	U38545	Hs.82587	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA complete cds
17483	3.7	AA122147	Hs.64691	ESTs
16854	3.7	AA055552	Hs.71622	ESTs Weakly similar to KIAA0319 [H.sapiens]
3709	3.7	U07550	Hs.1197	Heat shock 10 kD protein 1 (chaperonin 10)
1608	3.7	L00205	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D
4951	3.7	U69546	Hs.82321	Human RNA binding protein Etr-3 mRNA complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20418	3.6	N49209	Hs.32170	ESTs
27995	3.6	AA470155	Hs.75887	Homo sapiens coatomer protein (COPA) mRNA complete cds
7971	3.6	AA287423	Hs.126389	ESTs
27606	3.6	AA443793	Hs.94761	ESTs
24677	3.6	Z39338	Hs.21201	ESTs Highly similar to POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]
9328	3.6	D89618	Hs.3886	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds
17678	3.6	AA134275	Hs.134510	Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3
36209	3.6	AA421266	Hs.13889	ESTs Weakly similar to LIS-1 protein [H.sapiens]
20064	3.6	H98653	Hs.16056	ESTs
9713	3.6	L44338	Hs.78494	Homo sapiens mRNA for KIAA0525 protein partial cds
28622	3.6	D11837	Hs.29846	ESTs
28628	3.6	D11888	Hs.62386	ESTs Moderately similar to PROHIBITIN [H.sapiens]
25804	3.5	AA148885	Hs.111710	ESTs
2492	3.5	M22898	Hs.1846	Tumcr protein p53 (Li-Fraumeni syndrome)
14904	3.5	T83389	Hs.107147	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]
25265	3.5	AA043765	Hs.54649	H.sapiens RY-1 mRNA for putative nucleic acid binding protein
13606	3.5	AA456437	Hs.20386	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 kD SUBUNIT [H.sapiens]
42307	3.5	T96595	EST - RC_T96595	
1544	3.5	J05068	Hs.2012	TRANSCOBALAMIN I PRECURSOR
42311	3.5	T97257	Hs.94560	ESTs
2023	3.5	L34600	Hs.3823	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR
4540	3.5	U48807	Hs.2359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33707	3.5	Z39297	Hs.3281	Neuronal pentraxin II EST - RC_AA083070_s
17220	3.5	AA083070	Hs.18529	ESTs
24332	3.5	W85782	Hs.98117	ESTs
35887	3.5	AA412067	Hs.5101	Homc sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
8338	3.4	AA417152		
387	3.4	D28589	Hs.20890	ESTs
12319	3.4	AA398109	Hs.27437	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
15643	3.4	W58247		
11218	3.4	AA180488	Hs.33746	ESTs
16539	3.4	AA029328	Hs.1191	Human mRNA for KIAA0073 gene partial cds
29203	3.4	H28581	Hs.92711	ESTs
13838	3.4	AA465342	Hs.34045	ESTs
25585	3.4	AA112389	Hs.107932	H4(D10S170) Human-high-affinity copper uptake protein (HCTR1) mRNA complete cds
34018	3.4	AA191488	Hs.73614	
251	3.4	D14520	Hs.84728	Basic transcription element binding protein 2
3778	3.4	U09848	Hs.363	Zinc finger protein 139 (clone pHZ-37)
24535	3.4	Z38409	Hs.8053	ESTs
16127	3.4	AA004669	Hs.39441	ESTs
26149	3.4	AA250824	Hs.60478	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens] Human cysteine protease Mch2 isoform alpha (Mch2)
4011	3.4	U20536	Hs.3280	mRNA complete cds
5660	3.4	X16396	Hs.37791	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
26928	3.4	AA342580	Hs.47232	ESTs

**FIG.\_4Be**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36267	3.4	AA424046 R54726	Hs.98385 Hs.98493	ESTs DNA-REPAIR PROTEIN XRCC1
32257	3.4	AA101551	Hs.68900	ESTs
17365	3.4	W16684	Hs.74284	Moderately similar to <i>S.cerevisiae</i> hypothetical protein L3111 [H.sapiens]
15296	3.3			
17675	3.3	AA134064	Hs.44045	ESTs
10006	3.3	N81193	Hs.43133	Homo sapiens mRNA for KIAA0628 protein complete cds
33985	3.3	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
9570	3.3	H85169	Hs.24837	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds
37551	3.3	AA456679	Hs.7256	ESTs
18367	3.3	AA224180	Hs.93332	ESTs Moderately similar to ovarian-specific protein [R.noivegiicus]
14310	3.3	AA598412	Hs.8739	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION [Saccharomyces cerevisiae]
19233	3.3	H12634	Hs.8104	ESTs
12809	3.3	AA424406	Hs.31839	ESTs
21555	3.3	R33073	Hs.24595	EST
13767	3.3	AA463234	Hs.119387	ESTs
4738	3.3	U58766	Hs.75801	Human FX protein mRNA complete cds
7258	3.3	AA075427	Hs.17296	ESTs
17041	3.3	AA070364	EST - RC_AA070364	
15504	3.3	W28362	Hs.44131	ESTs
18214	3.3	AA196635	Hs.86081	
7401	3.3	AA094800	Hs.55682	Human translation initiation factor eIF3 p66 subunit mRNA complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18912	3.3	F10913	Hs.12475	Homo sapiens clone 23617 unknown mRNA partial cds
36317	3.3	AA425089	Hs.50722	Human mRNA for KIAA0334 gene complete cds
9410	3.3	H20443	Hs.31748	H.sapiens mRNA for TRE5
2146	3.2	L41390	EST .. L41390	
18683	3.2	F04258	Hs.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
33891	3.2	HUMTFRRI/M11507	AFFX-HUMTFRRI/M11507_M	
15840	3.2	X70944	Hs.91379	PTB-ASSOCIATED SPLICING FACTOR
3256	3.2	M92439	Hs.87157	130 KD LEUCINE-RICH PROTEIN
4400	3.2	U41387	Hs.5122	Human Gu protein mRNA partial cds
21350	3.2	R15846	Hs.21738	ESTs
11981	3.2	AA280928	Hs.24287	ESTs
23930	3.2	T96690	Hs.125123	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTFY !!! [H.sapiens]
30399	3.2	N45226	Hs.46495	EST
13494	3.2	AA453431	Hs.21043	ESTs
12908	3.2	AA427579	Hs.9347	ESTs
31309	3.1	N66818	Hs.42179	ESTs
31192	3.1	N64406	Hs.54174	ESTs
11288	3.1	AA196512	Hs.25916	ESTs
170	3.1	D00596	Hs.82962	Thymidylate synthase
26105	3.1	AA243133	Hs.48915	Homc sapiens serine/threonine kinase (BTAK) mRNA complete cds
11659	3.1	AA251909	Hs.36708	Homc sapiens MAD3-like protein kinase mRNA complete cds
19177	3.1	H10984	Hs.12338	ESTs
17380	3.1	AA102566	Hs.69149	ESTs
42397	3.1	W42928	Hs.103046	ESTs

**FIG.-4Bg**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14935	3.1	T94828	Hs.63220	ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]
3190	3.1	M86808	Hs.131361	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR
17406	3.1	AA112979	Hs.48269	Homo sapiens mRNA for VRK1 complete cds
14130	3.1	AA489041	Hs.15140	ESTs
14134	3.1	AA489080	Hs.3566	ESTs Highly similar to phosphorylation regulatory protein HP-1)[H.sapiens]
42421	3.1	W45491	Hs.106835	ESTs Weakly similar to T23G11.7 [C.elegans]
15723	3.1	W79060	Hs.5337	ESTs Highly similar to ribosome-binding protein p34 [R.norvegicus]
11140	3.1	AA158132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
14522	3.1	AA610108	Hs.27693	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schizosaccharomyces pombe]
15962	3.1	Z21420	Hs.30819	ESTs
13229	3.0	AA443811	Hs.23363	ESTs
27315	3.0	AA424038	Hs.58197	ESTs
35929	3.0	AA412429	Hs.48642	ESTs
17925	3.0	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein Gyr-rbp (GRY-RBP) mRNA complete cds
5053	3.0	U76992	Hs.71134	Human Tat-SF1 mRNA complete cds
15060	3.0	U54999	Hs.93121	Human LGN protein mRNA complete cds
17757	3.0	AA147224	Hs.71814	EST
26530	3.0	AA278650	Hs.73291	ESTs
22960		T10272	Hs.4287	ESTs

**FIG.-4Bh**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
4298	3.0	U36448	Hs.74574	Human Ca2+-dependent activator protein for secretion mRNA complete cds
7445	3.0	AA104023 AA179387	Hs.110048 ESTs	
18055	3.0	AA083339	Hs.73596 ESTs	
7282	3.0	D87009	Hs.126781 ESTs	
806	3.0	AA504255 R46837	Hs.43834 Human (lambda) DNA for immunoglobulin light chain Human protein kinase ATR mRNA complete cds	
38447	3.0	L19161	Hs.54404 ESTs	
41464	3.0	U82987	Hs.107450 Hs.121541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT Human Bcl-2 binding component 3 (bbc3) mRNA partial cds
9662	3.0	W93943	Hs.87246 ESTs	
15174	3.0	N95028	Hs.59509 ESTs	
33620	3.0	L24804	Hs.125031 ESTs	
41077	3.0	F03738	Hs.75839 ESTs	Human (p23) mRNA complete cds
1932	3.0	R40381	Hs.3657 ESTs	
39556	3.0	AA456646 AA281251	Hs.142852 ESTs	
32156	3.0	X68194	Hs.28661 ESTs	
13617	3.0	L00058	Hs.35696 ESTs	Weakly similar to trithorax protein trxII [D.melanogaster]
11989	3.0	U48705	Hs.80919 ESTs	Pantophysin [human keratinocyte line HaCaT mRNA 2106 nt]
6056	2.9	R56678	Hs.79070 ESTs	V-my: avian myelocytomatisis viral oncogene homolog
1605	2.9		Hs.75562 ESTs	Receptor protein-tyrosine kinase EDDR1
4536	2.9		Hs.102963 ESTs	Weakly similar to cell division control protein CDC21 [H.sapiens]
10173	2.9	N90401 AA421164	Hs.28928 ESTs	
21009	2.9	AA398622	Hs.107213 ESTs	
36200	2.9	M74558	Hs.75133 ESTs	Transcription factor G-like 1 (mitochondrial transcription factor 1-like)
35299	2.9		Hs.142965 ESTs	Human SII mRNA complete cds
9804	2.9			<b>FIG.-4Bi</b>

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12313	2.9	AA397916	Hs.22595	ESTs
5928	2.9	X62048	Hs.75188	WEE1-LIKE PROTEIN KINASE
18199	2.9	AA195318	Hs.63311	ESTs
19867	2.9	H61476	Hs.15641	ESTs
6081	2.9	X69398	Hs.82685	CD47 antigen (Rh-related antigen integrin-associated signal transducer)
5254	2.9	U86782	Hs.76887	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds
13579	2.9	AA455967	Hs.106705	Human neuronal PAS2 (NPAS2) mRNA complete cds
38495	2.9	AA505118	Hs.112255	Human nucleoporin 98 (NUP98) mRNA complete cds
2028	2.9	L35035	Hs.79886	RIBCSE 5-PHOSPHATE ISOMERASE
27374	2.9	AA425816	Hs.64641	ESTs Weakly similar to Y53C12A.3 [C.elegans]
26108	2.9	AA243189	Hs.53652	ESTs
4189	2.8	U30930	Hs.57700	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
16708	2.8	AA043944	Hs.62663	ESTs
357	2.8	D26156	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
26045	2.8	AA236276	Hs.87287	ESTs
8059	2.8	AA310967	Hs.5080	ESTs Weakly similar to T04A8.11 [C.elegansi]
21358	2.8	R16079	Hs.14775	ESTs
3572	2.8	S87759	Hs.57764	Protein phosphatase 2C alpha [human teratocarcinoma mRNA 2346 nt]
11877	2.8	AA262727	Hs.9591	ESTs
35830	2.8	AA411448	Hs.139386	ESTs
20151	2.8	N22895	Hs.6831	Hom sapiens clone 1400 unknown protein miRNA partial cds
38648	2.8	AA599267	EST - RC_AA599267	

**FIG.-4Bj**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7777	2.8	AA236820	Hs.118236	ESTs
32845	2.8	W31566	Hs.55459	EST
28258	2.8	AA505133	Hs.62273	ESTs
35944	2.8	AA412488	Hs.98150	ESTs
30648	2.8	N50971	Hs.42116	ESTs
8616	2.8	AA460077	Hs.28555	ESTs
34929	2.8	AA342084	EST .. RC_AA342084	
326	2.8	D21262	Hs.75337	Human mRNA for KIAA0035 gene partial cds
6480	2.8	X91788	Hs.84974	H.sapiens mRNA for lcdn protein
25202	2.8	AA034527	Hs.95182	EST
1681	2.8	L07493	Hs.1608	Replication protein A (E coli RecA homolog RAD51 homolog)
14566	2.8	AA621122	Hs.5198	ESTs
14182	2.8	AA490885	Hs.21766	ESTs
18253	2.7	AA206370	Hs.86248	ESTs
22911	2.7	T03865	Hs.27047	ESTs
35549	2.7	AA401274	Hs.31730	Hom <sub>c</sub> sapiens RRM RNA binding protein Gyr-rbp (GRY-RBP) mRNA complete cds
35955	2.7	AA412528	Hs.20183	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]
17642	2.7	AA132983	Hs.44155	ESTs Moderately similar to C-1-TETRAHYDROFOLATE
6131	2.7	X72841	Hs.2758	SYNTHASE CYTOPLASMIC [H.sapiens]
41429	2.7	R44994	Hs.108182	Human retinoblastoma-binding protein (RbAp46) mRNA complete cds
22937	2.7	T10065	Hs.4214	Homo sapiens TLS-associated protein TASR-2 mRNA complete cds

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
16243	2.7	AA012902	Hs.60556	ESTs
6444	2.7	X89750	Hs.90077	H.sapiens mRNA for TGIF protein
6240	2.7	X78627	Hs.75066	H.sapiens mRNA for translin
42116	2.7	T69924		EST - RC_T69924
7701	2.7	AA215333	Hs.97101	ESTs
17568	2.7	AA128905	Hs.22587	ESTs
42534	2.7	W73189	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds
29813	2.7	N21111	Hs.42946	ESTs
35273	2.7	AA398507	Hs.97361	ESTs
32563	2.7	T27697	Hs.21603	Human mRNA for KIAA0036 gene complete cds
13223	2.7	AA443720	Hs.7551	ESTs
8494	2.7	AA443460	Hs.3430	EST - HG3132-HT3308
1130	2.7	HG3132-HT3308		Human homeo box c1 protein mRNA complete cds
2379	2.7	M16937	Hs.819	Human SH3 domain-containing protein SH3P18 mRNA
18906	2.7	F10868	Hs.46571	complete cds
34796	2.7	AA291259	Hs.97101	ESTs
33688	2.7	Z38501	Hs.8768	ESTs Weakly similar to PROBABLE ES PROTEIN [Human papillomavirus type 58]
30733	2.7	N52078	Hs.13604	Homo sapiens mRNA for KIAA0637 protein complete cds
21256	2.7	R09195	Hs.86013	Homo sapiens mRNA for KIAA0564 protein partial cds
9296	2.7	D82775	Hs.10724	ESTs Weakly similar to unknown [S.cerevisiae]
3154	2.7	M83712	Hs.1614	Cholirergic receptor nicotinic alpha polypeptide 5
7383	2.7	AA093834	Hs.109822	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S.cerevisiae]
1923	2.7	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage elastase)

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30407	2.6	N45983	Hs.46572	ESTs
26286	2.6	AA253351	Hs.44439	ESTs
9558	2.6	H81497	Hs.12063	ESTs
18104	2.6	AA188801	Hs.85634	ESTs
8865	2.6	AB002359	Hs.105478	Human mRNA for KIAA0361 gene KIAA0361 protein
20422	2.6	N49300	Hs.24908	ESTs
41602	2.6	R67258	Hs.58215	ESTs Moderately similar to rhotekin [M.musculus]
4821	2.6	U62801	Hs.79361	Human protease M mRNA complete cds
16807	2.6	AA053296	Hs.63136	ESTs
15288	2.6	W07562	Hs.26198	ESTs Moderately similar to rA8 [R.norvegicus]
23822	2.6	T91715	Hs.14574	ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]
10951	2.6	AA126719	Hs.25282	ESTs
26891	2.6	AA292659	Hs.93667	ESTs
7699	2.6	AA215299	Hs.70830	Homo sapiens chromosome 19 cosmid R30783
11308	2.6	AA207114	Hs.27842	ESTs
4086	2.6	U24704	Hs.111709	Human antisecretory factor-1 mRNA complete cds
38615	2.6	AA598938	EST - RC_AA598938	
11819	2.6	AA258189	Hs.32471	ESTs
37433	2.6	AA454103	Hs.110031	ESTs
5587	2.6	X13482	Hs.80506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
19841	2.6	H59617	Hs.5199	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]
10655	2.6	AA040882	Hs.10290	ESTs
31574	2.6	N71303	Hs.50015	EST
7614	2.6	AA187579	Hs.102696	ESTs Weakly similar to Yel007c-ap [S.cerevisiae]

**FIG.\_4Bm**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7090	2.6	AA009913	Hs.103300	Homo sapiens diphthamide biosynthesis protein-2 (DPH2)
24219	2.6	W69960	Hs.19416	mRNA complete cds
19070	2.6	H05970	Hs.133828	ESTs
17719	2.6	AA136569	Hs.144295	Human clone 23960 mRNA sequence
11362	2.6	AA227261	Hs.20922	ESTs
8613	2.6	AA459555	Hs.31921	Homo sapiens mRNA for KIAA0648 protein partial cds
13866	2.6	AA476319	Hs.5327	PUTATIVE 60S RIBOSOMAL PROTEIN
39552	2.6	F03605	Hs.75574	Human chromosome 3p21.1 gene sequence complete cds
1795	2.6	L13434	Hs.84162	Human mRNA for KIAA0007 gene partial cds
14746	2.6	D60354	Hs.90315	Protein phosphatase 2 (formerly 2A) regulatory subunit B
2993	2.6	M64929	Hs.75200	(PR 52) alpha isoform
12986	2.6	AA430032	Hs.7487	ESTs Moderately similar to PTTG gene product [R.norvegicus]
18003	2.5	AA171692	Hs.70980	ESTs
42653	2.5	W92703	Hs.103239	ESTs
30438	2.5	N47204	Hs.46680	ESTs Weakly similar to C50F4.12 [C.elegans]
26135	2.5	AA243765	Hs.76977	ESTs
15457	2.5	W27560	Hs.90789	ESTs
27748	2.5	AA453159	Hs.41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA
32315	2.5	R69840	Hs.70189	complete cds
25310	2.5	AA046745	Hs.110457	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE
9658	2.5	L16991	Hs.79006	HOMOLOG [Nycticebus coucang]
12210	2.5	AA293774	Hs.21261	Deoxythymidylate kinase
				ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA
				SYNTHETASE MITOCHONDRIAL [C.elegans]

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**FIG.-4Bn**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
32826	2.5	W20391	Hs.20830	Human mRNA for kinesin-related protein partial cds
9692	2.5	L37747	Hs.89497	LAMIN B1
27862	2.5	AA458908	Hs.50883	ESTs
17288	2.5	AA085178	Hs.24382	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION
9888	2.5	N35449	Hs.111449	[Saccharomyces cerevisiae]
				Minichromosome maintenance deficient ( <i>S. cerevisiae</i> ) 3
5932	2.5	X62153	Hs.82479	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE
26834	2.5	AA287138	Hs.59346	[ <i>Thermus aquaticus</i> thermophilus]
5157	2.5	U80034	Hs.68583	Human mitochondrial intermediate peptidase precursor (MIEP) mRNA  mitochondrial gene encoding mitochondrial protein complete cds
38434	2.5	AA497013	Hs.142592	ESTs
7590	2.5	AA173505	Hs.35353	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHC2-POL3 INTERGENIC REGION [ <i>S.cerevisiae</i> ] Human fetal Alz-50-reactive clone 1-(FAC1) mRNA complete cds
14960	2.5	U05237	Hs.99872	[Sus sc. ofa]
13585	2.5	AA455999	Hs.22151	ESTs Highly similar to NEUROLYSIN PRECURSOR Homo sapiens mRNA for KIAA0688 protein complete cds
38185	2.5	AA487508	Hs.9877	Annexin XI (56kD autoantigen)
34678	2.5	AA284744	Hs.75510	Eukaryotic translation initiation factor 2A
1424	2.5	J02645	Hs.81613	EST - RC_R43286
21876	2.5	R43286	Hs.111314	ESTs
34290	2.5	AA236866	Hs.58169	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds
18109	2.5	AA188981		

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
6485	2.5	X92098	Hs.75914	H.sapiens mRNA for transmembrane protein rmp24
27444	2.5	AA430160	Hs.42785	ESTs Weakly similar to F25H9.7 [C.elegans]
30037	2.5	N27439	Hs.51652	ESTs
27602	2.5	AA443702	Hs.29835	ESTs Weakly similar to W02B12.7 [C.elegans]
3390	2.5	S59184	Hs.79350	RYK receptor-like tyrosine kinase
25040	2.5	AA010188	Hs.103305	ESTs
40477	2.4	N24006	Hs.99348	Homo sapiens BAC clone RG300E22 from 7q21-q31.1
18620	2.4	F02506	Hs.9417	ESTs
15120	2.4	U73524	Hs.87465	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds
28813	2.4	D59257	Hs.91161	Human C-1 mRNA complete cds
34723	2.4	AA287115	Hs.99697	ESTs
7960	2.4	AA285277	Hs.8932	Homo sapiens brain expressed ring finger protein mRNA complete cds
18927	2.4	F11087	Hs.12544	ESTs
28443	2.4	AA621611	Hs.70877	RAN binding protein 1.
452	2.4	D38076	Hs.24763	Homo sapiens RRM RNA binding protein Gry-rbp
11701	2.4	AA253031	Hs.31730	(GRY-RBP) mRNA complete cds
12672	2.4	AA417067	Hs.13055	ESTs
4836	2.4	U63717	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
42200	2.4	T83729	EST- FC_T83729	
28395	2.4	AA610064	Hs.73602	ESTs
36390	2.4	AA426291	Hs.108527	ESTs Weakly similar to No definition line found [C.elegans]
12916	2.4	AA427745	Hs.37747	ESTs
36786	2.4	AA435815	Hs.77965	Human Clk-associated RS cyclophilin CARS-Cyp mRNA complete cds

**FIG.-4Bd**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39462	2.4	D60063	Hs.9012	ESTs
14420	2.4	AA600322	Hs.19574	ESTs Highly similar to AAC-RICH mRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]
27431	2.4	AA429038	Hs.40541	ESTs
6387	2.4	X85372	Hs.105465	H.sapiens mRNA for Sm protein F
11342	2.4	AA223874	Hs.14843	Homo sapiens mRNA for KIAA0704 protein partial cds
1497	2.4	J04088	Hs.3378	Topoisomerase (DNA) II alpha (170kD)
11454	2.4	AA233854	Hs.23348	ESTs
32978	2.4	W42788	Hs.1098	Human terminal transferase mRNA complete cds
27872	2.4	AA459254	Hs.48855	ESTs
11623	2.4	AA243617	Hs.31082	ESTs
22142	2.4	R51382	Hs.124275	Homo sapiens mRNA for KIAA0659 protein partial cds
13533	2.4	AA454607	Hs.38114	ESTs Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]
6231	2.4	X78121	Hs.2010	Choriopteremia
24371	2.4	W87415	Hs.16918	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
25286	2.4	AA045261	Hs.108259	ESTs
8163	2.4	AA357394	Hs.98073	ESTs
12233	2.4	AA343513	Hs.28813	ESTs Weakly similar to LINE/Ig H-chain fusion protein [M.musculus]
14371	2.4	AA599219	Hs.30272	ESTs Moderately similar to ALR [H.sapiens]
26169	2.4	AA251089	Hs.94576	ESTs Weakly similar to ORF YOR281c [S.cerevisiae]
23065	2.4	T23539	Hs.7165	ESTs Highly similar to zinc finger protein [M.musculus]
20524	2.4	N53965	Hs.15741	ESTs
20837	2.4	N69263	Hs.20524	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]
21195	2.4	R07210	Hs.19913	ESTs

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
13377	2.4	AA449720	Hs.20201	Homo sapiens clone 24706 mRNA sequence
17352	2.3	AA100925	Hs.20990	ESTs
11914	2.3	AA278907	Hs.24549	ESTs
28796	2.3	D51272	Hs.29055	EST - RC_D51272_s
22491	2.3	R70012	Hs.109437	ESTs
40847	2.3	N66354	Hs.19582	Homo sapiens mRNA for hTCF-4
42022	2.3	T53138	Hs.109957	ESTs
8053	2.3	AA309880	Hs.123058	Human mRNA for RNA helicase complete cds
363	2.3	D26528	Hs.4310	ESTs
26679	2.3	AA281733	Hs.54642	EST
31858	2.3	N90680	Hs.14611	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
24092	2.3	W42845	Hs.31942	EST
19428	2.3	A418389	Hs.42219	ESTs
27264	2.3	AA456286	Hs.30794	ESTs
13600	2.3	AA454943	Hs.29911	ESTs
13552	2.3	AA279774	Hs.142497	ESTs
26583	2.3	U05237	Hs.99872	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds
36744	2.3	Z38770	Hs.71623	ESTs
33694	2.3	AA064616	Hs.66983	ESTs
16977	2.3	X63337	EST - X63337	
5948	2.3	W73010	Hs.108761	Ribosomal protein L37
24247	2.3	N67816	Hs.53263	ESTs Moderately similar to !!! ALU SUBFAMILY SX
40879	2.3			WARNING ENTRY !!! [H.sapiens]

FIG.-4Br

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5875	2.3	X59405	Hs.83532	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)
9239	2.3	D79100	Hs.83196	ESTs
41997	2.3	T47788	Hs.109628	ESTs
39565	2.3	F04320	Hs.35120	Replication factor C 37-kD subunit
7404	2.3	AA094989	Hs.7381	Homo sapiens voltage dependent anion channel protein mRNA complete cds
6388	2.3	X85373	Hs.77496	H.sapiens mRNA for Sm protein G
14529	2.3	AA620307	Hs.27379	ESTs
21197	2.3	R07320	Hs.19936	ESTs
28203	2.3	AA490969	Hs.59838	ESTs
38320	2.3	AA490611	Hs.99838	ESTs
4674	2.3	U54999	Hs.93121	Human LGN protein mRNA complete cds
26756	2.3	AA283832	Hs.86619	ESTs
11567	2.3	AA236747	Hs.30327	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds
25050	2.3	AA011134	Hs.25863	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
26895	2.3	AA292765	Hs.42650	H.sapiens mRNA for M-phase phosphoprotein mpp5
3343	2.3	M97936	Hs.21486	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
42435	2.3	W46994	Hs.109903	ESTs
5937	2.2	X62534	Hs.80684	High-mobility group (nonhistone chromosomal) protein 2
25756	2.2	AA135868	Hs.95783	ESTs
34184	2.2	AA227959	Hs.3280	Human cysteine protease Mcch2 isoform alpha (Mcch2)
8672	2.2	AA477046	Hs.59838	mRNA complete cds
				ESTs

FIG.-4Bs

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7387	2.2	AA093977 AA173223 N69352	Hs.71475 Hs.44426 Hs.5683	ESTs ESTs Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds
18016	2.2			
20843	2.2			
10054	2.2	R10266	Hs.120997	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAAC2 INTERGENIC REGION [Saccharomyces cerevisiae]
34094	2.2	AA206088 R27296	Hs.104139 Hs.23240	ESTs ESTs
41246	2.2	R82837	Hs.103329	ESTs
22634	2.2	H48502	Hs.28212	ESTs
19686	2.2	AA621752	Hs.76887	Human 26S proteasome-associated pad1 homolog (POH1) mRNA:complete cds
28448	2.2	D78129 N29345	EST - [D]78129 Hs.28917	ESTs CDC28 protein kinase 1
651	2.2	X54941	Hs.77550	Human Gu protein mRNA partial cds
20221	2.2	D19708	Hs.5122	ESTs
5792	2.2	H13265	Hs.31196	Human 26S proteasome-associated pad1 homolog (POH2) mRNA:complete cds
28656	2.2	AA252672	Hs.103300	ESTs
19240	2.2			
11688	2.2			
14152	2.2	AA489790	Hs.4976	Homo sapiens Ran-GTP binding protein mRNA partial cds
38341	2.2	AA490967	Hs.105276	ESTs
11803	2.2	AA257971	Hs.21214	ESTs
39085	2.2	AA620599	Hs.24766	ESTs
4046	2.2	U22376	Hs.1334	MYB Proto-oncogene protein
11600	2.2	AA242868	Hs.7395	ESTs Weakly similar to house-keeping protein [M.musculus]

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5051	2.2	U76638	Hs.54089	Human BRCAl-associated RING domain protein (BARD1) mRNA complete cds
20674	2.2	N63392	Hs.128003	ESTs
41031	2.2	N91246	Hs.102897	ESTs
24711	2.2	Z39645	Hs.21470	ESTs
4733	2.2	U58658	Hs.57689	Human unknown protein mRNA within the p53 intron 1 complete cds
29733	2.2	H99398	Hs.42680	EST
23155	2.2	T30550	Hs.22615	ESTs
346388	2.2	AA282987	Hs.104473	EST
1889	2.2	L20591	Hs.1378	Annexin III (lipocortin III) ICH-2 PROTEASE PRECURSOR
4136	2.2	U28014	Hs.74122	ESTs
20276	2.2	N32919	Hs.27931	ESTs
18238	2.2	AA205389	Hs.41145	ESTs
13250	2.1	AA446459	Hs.27599	ESTs
34370	2.1	AA251829	Hs.104058	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MEF2-CPR7 INTERGENIC REGION [Saccharomyces cerevisiae]
27996	2.1	AA470156	Hs.80449	ESTs Weakly similar to dynein 74K chain cytosolic [R.norvegicus]
10804	2.1	AA069549	Hs.18479	ESTs
34552	2.1	AA279985	Hs.18389	Human mRNA for KIAA0372 gene complete cds
18380	2.1	AA227119	Hs.70256	ESTs
37415	2.1	AA453807	Hs.99349	ESTs
14582	2.1	AA621340	Hs.10600	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
5173	2.1	U81554	Hs.5171	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds
19972	2.1	H83639	Hs.33576	ESTs
23301	2.1	T52847	Hs.13034	ESTs
20504	2.1	N52966	Hs.142838	ESTs
40145	2.1	H81391	Hs.81182	Human mRNA for histamine N-methyltransferase complete cds
34611	2.1	S75256	EST - S75256	
41893	2.1	T23611	Hs.51251	ESTs
36021	2.1	AA416876	Hs.5169	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens]
5807	2.1	X55740	Hs.76856	5' nucleotidase (CD73)
38155	2.1	AA486777	Hs.105698	ESTs
924	2.1	HG1112-HT1112	EST - HG1112-HT1112	
8384	2.1	AA424282	Hs.91728	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds
25165	2.1	AA027837	Hs.30705	Retinitis pigmentosa 3 (X-linked recessive)
24348	2.1	W86469	Hs.77899	Tropomyosin alpha chain (skeletal muscle)
35340	2.1	AA398900	EST - FIC_A398900	
10898	2.1	AA112063	Hs.15313	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]
381	2.1	D28473	Hs.78770	Isoleucine-tRNA synthetase
22051	2.1	R49047	Hs.31975	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
11528	2.1	AA236018	Hs.10724	ESTs Weakly similar to unknown [S.cerevisiae]
11890	2.1	AA278323	Hs.17481	Homo sapiens clone 24606 mRNA sequence
5448	2.1	X02751	Hs.69855	Neuroblastoma RAS viral (v-ras) oncogene homolog
35956	2.1	AA412533	Hs.109571	ESTs
7525	2.1	AA149259	Hs.69851	ESTs

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		UNIGENE CLUSTER	UNIGENE ID	UNIGENE DESCRIPTOR
			UNIGENE CLUSTER	UNIGENE ID			
39592	2.1	F09351		Hs.16492	ESTs Weakly similar to weakly similar to <i>S. cervisiae</i> PTM1 precursor [C.elegans]		
28029	2.1	AA478479	Hs.71992				
18425	2.1	AA232103	Hs.59112				
33368	2.1	W80814	Hs.47283				
20590	2.1	N58146	Hs.34227				
12907	2.1	AA427577	Hs.26502				
22958	2.1	T10264	Hs.116122				
39	2.1	AB003698	Hs.28853				
14350	2.1	AA598831	Hs.17121				
25593	2.1	AA113149	Hs.8130				
26529	2.1	AA278594	Hs.88461				
6681	2.1	Y00971	Hs.2910				
16879	2.1	AA056538	Hs.63314				
38040	2.1	AA481403	Hs.107213				
4111	2.1	U26312	Hs.83550				
32878	2.1	W37448	Hs.41241				
25968	2.1	AA234935	Hs.65032				
24659	2.1	Z39211	Hs.12299				
38030	2.1	AA481148	Hs.105157				
61	2.0	AC002115	Hs.83379				
37681	2.0	AA460675	Hs.31748				
27125	2.0	AA405505	Hs.48295				
3780	2.0	U09851	Hs.112180				
9112	2.0	D16611	Hs.89866				

**FIG. 4BW**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7519	2.0	AA147425	Hs.124852	EST - AA147425_s
14701	2.0	D59324	ESTs	
380	2.0	D28423	EST - [D28423	
825	2.0	D87328	Hs.79375	Holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing) ligase)
3997	2.0	U19906	Hs.2131	Arginine vasoressin receptor 1 (AVPR1)
377	2.0	D28364	EST - [D28364	
28379	2.0	AA609710	Hs.42582	ESTs Weakly similar to The KIAA0138 gene product is novel.
7322	2.0	AA090692	Hs.135552	[H.sapiens]
29358	2.0	H70641	ESTs	
24230	2.0	W72276	Hs.5950	
40212	2.0	H88535	Hs.9564	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence
36319	2.0	AA425107	Hs.97016	ESTs
25654	2.0	AA126951	Hs.110857	ESTs Weakly similar to DNA-directed RNA polymerase [D.melanogaster]
16344	2.0	AA018907	Hs.5427	ESTs
8118	2.0	AA328993	Hs.104558	
29962	2.0	N25228	Hs.27349	
32236	2.0	R49327	Hs.57435	Natural resistance-associated macrophage protein 2
37972	2.0	AA479215	EST - RC_AA479215	
34834	2.0	AA292655	Hs.96557	ESTs

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens mRNA for I-15P (I-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPROPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M19828	Hs.585	Apolipoprotein B (including Ag(X) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-II/uroguanylin precursor
1304	>10	HG4310	EST - HG4310-HT4580	
5980	>10	X64559	Hs.65424	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA-CHAIN [Mus]
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65577	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28264	ESTs
41148	>10	R06984	EST - RC_R06984_S	
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
4605	>10	U51010	EST - U51010	
28359	>10	AA609133	Hs.58115	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
19537	>10	H30270	Hs.32583	ESTs
18784	>10	F09748	Hs.7974	ESTs
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1
27387	>10	AA426330	Hs.78264	ESTs
2866	>10	M59815	Hs.76682	Complement component 4A
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds
7026	>10	Z80345	Hs.127610	Acy-Coenzyme A dehydrogenase C-2 to C-3 short chain
16736	>10	AA045306	Hs.42996	ESTs
4630	>10	U52101	Hs.9999	Human YMP mRNA complete cds
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
42758	>10	Z41411	Hs.107040	ESTs
35637	>10	AA402933	Hs.29283	ESTs
40392	>10	H99587	Hs.108880	ESTs
7354	>10	AA092348	Hs.7858	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9034	>10	C01833	Hs.29759	ESTs Weakly similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
9003	>10	C00808	Hs.107882	ESTs
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha
21934	>10	R44449	Hs.48778	ESTs
11129	8	AA156873	Hs.15970	ESTs
40387	7	H99460	Hs.108873	ESTs

FIG.-5Ac

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2348	>10	M15656	Hs.75592	Aldolase 3 fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens: mRNA for I-15P (I-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens: mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M119828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	H.sapiens: mRNA for GCAP-II/uroguanylin precursor
7006	>10	Z70295	Hs.32966	EST - HG4310-HT4580
1304	>10	HG4310-		Tetranectin (plasminogen-binding protein)
5980	>10	X64559	Hs.65424	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase)
41987	>10	T47089	Hs.121713	congenital adrenal hyperplasia
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M116594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28264	ESTs
41148	>10	R06984		EST - RC_R06984_S
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T68873	Hs.143289	H.sapiens mRNA for metallothionein isoform 1R
4605	>10	U51010		EST - U51010
28359	>10	AA609133	Hs.58115	ESTs

*FIG.-6Aa*

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194 AA284767	Hs.80552 Hs.21910	ESTs
12084	>10	R48732	Hs.11006	ESTs
41473	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
32568	>10			
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N64436	Hs.20813	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403032	Hs.21701	ESTs
42059	>10	T61654	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
25468	>10	AA079072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs
16938	>10	AA059473	Hs.66783	ESTs
41788	>10	T03735	Hs.26885	ESTs
7754	>10	AA234634	Hs.76722	Human N-IL6-beta protein mRNA complete cds
6122	>10	X72012	Hs.75962	Endoglin (Osler-Rendu-Weber syndrome 1)
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
23013	>10	T16661	Hs.6725	ESTs
19537	>10	H30270	Hs.32583	ESTs
4584	>10	U50360	EST - U50360	
37410	>10	AA453652	Hs.99344	ESTs
27969	>10	AA464594	Hs.63382	ESTs
35497	>10	AA400606	Hs.144344	EST

**FIG.-6Ab**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37013	>10	AA443690	Hs.136268	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]
39247	>10	AA621553	Hs.112998	ESTs
13471	>10	AA452598	Hs.109590	ESTs
42110	>10	T68878	Hs.76688	Carboxylesterase 2 (liver)
10965	>10	AA128997	Hs.18953	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds
4918	>10	U67733	Hs.3831	Human cGMP-stimulated 3'5'-cyclic nucleotide phosphodiesterase PDE2A3 [PDE2A] mRNA complete cds
40737	>10	N54950	Hs.81454	H.sapiens: KHK mRNA for ketohexokinase clone pHKHK3a
30403	>10	N45300	Hs.110647	Meis1 (mouse) homolog
11432	>10	AA233369	Hs.361	ESTs
18784	>10	F09748	Hs.7974	ESTs
40662	>10	N49281	EST - RC_N49281	EST - RC_N49281
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1
35041	>10	AA350586	Hs.30862	ESTs
20868	>10	N70068	Hs.7243	ESTs
39729	>10	H11489	Hs.105805	ESTs
27387	>10	AA426330	Hs.78264	ESTs
39758	>10	H15814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds
4319	>10	U37283	Hs.58882	Human microfibril-associated glycoprotein-2 MAGP-2 mRNA complete cds
2866	>10	M59815	Hs.76682	Complement component 4A
30332	>10	N39075	Hs.44934	EST
41344	>10	R40189	Hs.6985	ESTs

FIG.-6Ac

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28271 5834	>10 >10	AA521200 X57129	Hs.48778 Hs.7644	ESTs HISTONE: H1D
19048 1429	>10 >10	H05464 J02854	Hs.100251 Hs.9615	ESTs Human 21)-kDa myosin light chain (MLC-2) mRNA complete cds
19491 29992	>10 >10	H27910 N26386	Hs.107384 Hs.33084	ESTs Solute carrier family 2 (facilitated glucose transporter) member 15
2041 22865	>10 >10	L36033 R99909	Hs.77423 Hs.36186	Stromal cell-derived factor 1 ESTs
11624 12512	>10 >10	AA243654 AA405199	Hs.17998 Hs.20733	ESTs ESTs
41443 5055	>10 >10	R45577 U77180	Hs.10683 Hs.50002	ESTs Human m RNA for EBI1-ligand chemokine complete cds
6038	>10	X66945	Hs.7448	Basic fibroblast growth factor (bFGF) receptor (shorter form)
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	>10	D87433	Hs.84753	Human m RNA for KIAA0246 gene partial cds
650	>10	D78014	Hs.74566	Human m RNA for dihydropyrimidinase related protein-3 complete cds
37350 37488	>10 >10	AA452606 AA455178	Hs.99289 Hs.99397	EST ESTs
36646 38999	>10 >10	AA431797 AA609907	Hs.98763	EST
38191 9944	>10	AA487895 N57464	Hs.17311 Hs.74670	ESTs - RC_AA609907 Human m RNA for KIAA0146 gene partial cds
8139 41522	>10 >10	AA341723 R53966	Hs.107374 Hs.75092	ESTs N-CHIMAERIN

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
		ACCESSION	
38090	>10	AA482603	Hs.111301 Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase) EST - R_C_R09241
41175	>10	R09241	ESTs
36947	>10	AA437388	Pigment epithelium-derived factor EST
41175	>10	U29953	Xanthine dehydrogenase EST
35421	>10	AA399686	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain EST
4358	>10	U39487	Homo sapiens clone 24519 unknown mRNA partial cds EST
35463	>10	AA400272	Hs.97758 EST
7026	>10	Z80345	Hs.127610 ESTs
34625	>10	AA282238	Hs.118463 ESTs
20179	>10	N24879	Hs.9693 ESTs
36805	>10	AA435901	Hs.56874 ESTs
24447	>10	W93121	Hs.23841 ESTs
10247	>10	R74386	Hs.108924 ESTs
36118	>10	U02388	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF) ESTs
1464	>10	J03474	SERUM AMYLOID A PROTEIN PRECURSOR ESTs
16842	>10	AA055163	Homo sapiens mRNA for cardiac calsequestrin complete cds ESTs
16736	>10	AA045306	ESTs
22666	>10	R85880	ESTs
5248	>10	U86358	Human chemokine (TECK) mRNA complete cds ESTs
7510	>10	AA136353	ESTs
34683	>10	AA284920	ESTs
19986	>10	H89980	Moderately similar to protein phosphatase 1 binding protein PTG [M.rnuscus] ESTs
9959	>10	N75215	Hs.43148

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38136	>10	AA486185	Hs.125176	ESTs
36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
3357	>10	M99487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36783	>10	AA435805	Hs.112065	EST
4876	>10	U66061	Hs.2048	Protease :serine 2 (trypsin 2)
41149	>10	R06986	Hs.76487	ESTs
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin
12944	>10	AA428258	Hs.8769	ESTs
9317	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
19331	>10	H17865	Hs.23213	ESTs
5032	>10	U74382	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
34239	>10	AA235009	Hs.32246	ESTs
32852	>10	W31906	Hs.116428	ESTs
6432	>10	X89066	Hs.94413	Transient receptor potential channel 1
37001	>10	AA443311	Hs.98998	ESTs
4630	>10	U52101	Hs.9999	Human YM/P mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs
23028	>10	T17215	Hs.6952	ESTs
35359	>10	AA399061	Hs.112961	Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235984	Hs.87469	ESTs
41348	>10	R40395	Hs.112125	Lecithin-cholesterol acyltransferase
14494	>10	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]

FIG.-6Af

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
4453	>10	U43916	Hs.79368	Human epithelial membrane protein(CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
35637	>10	AA402933	Hs.29283	ESTs
40392	>10	H99587	Hs.108880	ESTs
19366	>10	H19204	Hs.133466	ESTs
5184	>10	U82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
859	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
1595	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.26216	ESTs
8985	>10	C00125	Hs.24332	ESTs Weakly similar to similar to deoxyribose-phosphate aldolase [C.elegans]
33995	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds
7949	>10	AA283620	Hs.34956	ESTs
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
7354	>10	AA092348	Hs.7858	ESTs
36151	>10	AA419011	Hs.96744	ESTs
42136	>10	T72491	Hs.73849	Apolipoprotein C-III
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0673 protein partial cds
34764	>10	AA287870	Hs.890	Lymphotoxin-beta
24515	>10	Z38289	Hs.12701	ESTs
18652	>10	F03111	Hs.22505	ESTs

*FIG.-6Aa*

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37815 9034	>10 >10	AA469952 C01833	Hs.97899 Hs.29759	ESTs ESTs Weakly similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]
34805 12246 42153 27110 28831 63333 10935 27257  3631	>10 >10 >10 >10 >10 >10 >10 >10 >10	AA291522 AA348198 T77729 AA404494 D59722 X82494 AA121534 AA418001  U03090	Hs.97250 Hs.14829 Hs.89890 Hs.84112 Hs.92924 Hs.2653 Hs.6923 Hs.46146  Hs.290	EST Homo sajiens mRNA for GABA-BR1a (hGB1a) receptor Pyruvate carboxylase CTP synthetase ESTs Fibulin 2 ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus] ESTs Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens] Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds Glycoprotein Ib (platelet) beta polypeptide CYCLIN-D1)DEPENDENT KINASE INHIBITOR 1 Macrophege stimulating 1 (hepatocyte growth factor-like) ESTs Integrin alpha 5 (fibronectin receptor alpha polypeptide) ESTs ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58KD isoform 1 Glutathione S-transferase M2 (muscle) Human clone HM18 monocyte inhibitory receptor precursor mRNA complete cds
4752 3766 4310 26923 5520 16720 25336 2547  9796 5206	>10 >10 >10 >10 >10 >10 >10 >10  >10 >10	U59632 U09579 U37055 AA342302 X06256 AA044732 AA053405 M25809  M63509 U82979	Hs.3847 Hs.74984 Hs.76034 Hs.55036 Hs.119218 Hs.77208 Hs.101404 Hs.1009  Hs.73974 Hs.67846	

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PRIMARY KEY	FOLD DOWNREGULATED	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9377	>10	H12674	Hs.9396	ESTs
41960	>10	T33511	Hs.4844	ESTs
21911	>10	R43980	Hs.26320	ESTs
16225	>10	AA011305	Hs.10029	Cathepsin C
16071	>10	AA001426	Hs.40863	ESTs
29335	>10	H68239	Hs.39122	ESTs
34966	>10	AA344866	Hs.1285	Complement component 8 gamma polypeptide
21076	>10	N99976	Hs.8016	ESTs
4402	>10	U41518	Hs.74602	AQUAPCRIN-CHIP
20423	>10	N49308	Hs.104938	ESTs
16575	>10	AA031948	Hs.57548	ESTs
28264	>10	AA521080	Hs.46765	ESTs
9003	>10	C00808	Hs.107882	ESTs
5632	>10	X15357	EST - X15357	
20852	>10	N69540	Hs.17713	ESTs
34585	>10	AA281002	Hs.40735	ESTs
33690	>10	Z38607	Hs.62248	ESTs
8904	>10	AF002256	Hs.86180	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds
3307	>10	M95809	Hs.89578	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT
39200	>10	AA621246	Hs.112956	EST
24712	>10	Z39652	Hs.27457	
2199	>10	L49169	Hs.75678	Human GOS3 mRNA complete cds
38942	>10	AA609646	Hs.94970	Human mRNA for KIAA0306 gene partial cds
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha
6834	>10	Z18954	Hs.2960	S100 calcium-binding protein A5 (formerly S100D)

**FIG.-6Ai**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40562	>10	N33212	Hs.107197	ESTs
37333	>10	AA452158	Hs.75122	TRANSFORMING PROTEIN RHOB
3992	>10	U19713	Hs.76364	Allograft inflammatory factor 1
38734	>10	AA608792	Hs.112591	EST
37836	>10	AA470135	Hs.112238	ESTs
10000	>10	N79674	Hs.7915	ESTs
30658	>10	N51105	Hs.111223	ESTs
17629	>10	AA131919	Hs.69009	ESTs
36260	>10	AA423970	Hs.98378	ESTs
24122	>10	W46947	Hs.4188	ESTs
1066	>10	HG2705-	EST - HG2705-HT2801	
12389	>10	AA399633	Hs.24872	ESTs
26025	>10	AA235874	Hs.888888	PUTATIVE DNA BINDING PROTEIN A20
41104	>10	R01398	EST - RC_R01398	
33586	>10	W93015	Hs.73166	Treacher Collins syndrome susceptibility protein
25379	>10	AA058893	Hs.111841	Human adenylyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds
17907	>10	AA160530	Hs.72447	ESTs
36838	>10	AA436163	Hs.95851	Homo sapiens Pig12 (PIG12) mRNA complete cds
19524	>10	H29566	Hs.83466	Homo sapiens clone 23579 mRNA sequence
21934	>10	R44449	Hs.48778	ESTs
32456	>10	T15829	Hs.65264	ESTs
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonospora curvata]
2807	>10	M55210	Hs.87428	Laminin gamma 1 (formerly LAMB2)
34193	>10	AA232251	Hs.128630	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	CLUSTER	UNIGENE DESCRIPTOR
14584	>10	AA621414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds EST
38752	>10	AA608852	Hs.112603	
5294	>10	U90065	Hs.79351	Human two P-domain K+ channel TWIK-1 mRNA complete cds
84	>10	AF001359		EST - AF001359_f
4856	>10	U65093	Hs.82071	Human msg1-related gene 1 (mrg1) mRNA complete cds
13974	>10	AA479299	Hs.21107	ESTs
26151	>10	AA250836	Hs.108509	ESTs
5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80kD)
17717	>10	AA136541	Hs.711647	EST
12404	>10	AA400292	Hs.23786	ESTs
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR
26620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncogene sp1
37675	10	AA460377	Hs.99816	ESTs
41827	10	T15445	Hs.99491	H.sapien: mRNA for F25B3.3 kinase like protein from C.elegans
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
203	10	D12620	Hs.106242	CYTOCHROME P450 IVF3
24159	10	W57862	Hs.21289	ESTs
5302	10	U90543	Hs.79041	Human b-tyrophilin (BTTF1) mRNA complete cds
2219	10	L76670	Hs.109610	Homo sapiens nkat7 mRNA complete cds
24392	10	W88568	Hs.58589	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds
36159	10	AA419279	Hs.82813	Colony-stimulating factor 1 (M-CSF)
28251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK792.1 [C.elegans]
37592	10	AA458668	Hs.95898	ESTs
39619	9	F10640	Hs.12354	ESTs

**FIG.-64K**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
8240	9	AA397841	Hs.106879	ESTs
10887	9	AA101632	Hs.22971	ESTs
37500	9	AA455474	Hs.100530	ESTs
42650	9	W92272	Hs.25601	Homo sapiens zinc-finger helicase (hZFH) mRNA complete cds
9011	9	C01394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
36691	9	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
3478	9	S76992	Hs.104005	Vav 2 oncogene
42034	9	T56281	Hs.110440	Human metallothionein (MT)I-F gene
11845	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]
42395	8	W42733	Hs.109870	ESTs
11425	8	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds
15310	8	W19098	Hs.7921	ESTs
36601	8	AA431337	Hs.98017	ESTs
13499	8	AA453458	Hs.7301	ESTs
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1
5998	8	X65644	Hs.75063	HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2
33589	8	W93074	Hs.59342	ESTs
5801	8	X55448	Hs.3118	H.sapiens mRNA for 2.19 gene
11129	8	AA156873	Hs.15970	ESTs
31987	8	N94551	Hs.55060	ESTs
40438	8	N21684	Hs.80500	Human mRNA for KIAA0061 gene partial cds
34471	8	AA258843	Hs.111376	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25530	8	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
39471	7	D60265 AA019426	Hs.107894 Hs.103343	ESTs EST
25100	7	Y09858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical protein E
15915	7			ESTs
19097	7	H08171	Hs.30842	ESTs
35353	7	AA398962 AA435978	Hs.97699 Hs.98852	EST
36822	7	AA400893	Hs.41717	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds
35530	7			Human F1al guanine nucleotide dissociation stimulator mRNA partial cds
3869	7	U14417	Hs.106185	Solute carrier family 5 (sodium/glucose cotransporter) member 1
1979	7	L29339	Hs.1964	Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA complete cds
26178	7	AA251153	Hs.27910	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds
36428	7	AA427605	Hs.98551	Homo sapiens regulator of G protein signaling 10 mRNA complete cds
26333	7	AA256075	Hs.82280	ESTs
40387	7	H99460 AA417037	Hs.108873 Hs.67805	ESTs
27236	7	H99879	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]
20083	7			

**FIG.-6Am**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR	
21561	7	R33245	Hs.23076	ESTs	Homo sapiens chromosome 19 cosmid F22329
21223	7	R08175	Hs.110130	ESTs	Homo sapiens chromosomal fragment
13405	7	AA450118	Hs.25722	ESTs	Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]
34845	7	AA293420	Hs.95464	ESTs	Moderately similar to transcription enhancer factor TEF1-[H.sapiens]
15059	7	U53831	Hs.85280	Human interferon regulatory factor 7 (hurnirf7) mRNA complete cds	Human interferon regulatory factor 7 (hurnirf7) mRNA complete cds
1945	7	L25878	Hs.89649	Epoxide hydrolase 1 microsomal (xenobiotic)	Epoxide hydrolase 1 microsomal (xenobiotic)
42648	7	W92150	Hs.79310	Human G <i>i</i> AP SH3 binding protein mRNA complete cds	Human G <i>i</i> AP SH3 binding protein mRNA complete cds
20041	7	H97012	Hs.11050	ESTs	Weakly similar to L8004.7 gene product [S.cerevisiae]
7053	6	Z84721	Hs.75792	Hemoglobin alpha 1	Hemoglobin alpha 1
23843	6	T92561	Hs.110422	ESTs	
25815	6	AA149889	Hs.96200	ESTs	Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]
8473	6	AA437346	Hs.2967	SHB adaptor protein (a Src homology-2 protein)	SHB adaptor protein (a Src homology-2 protein)
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA	H.sapiens mRNA for melanoma growth regulatory protein MIA
11074	6	AA148983	Hs.29068	ESTs	
17533	6	AA127098	Hs.71057	EST	
28973	6	F04014	Hs.65996	ESTs	
17042	6	AA070397		EST - RC: AA070397	
15246	6	W01094	Hs.84628	ESTs	
2247	6	M10321	Hs.110802	VON WILLEBRAND FACTOR PRECURSOR	VON WILLEBRAND FACTOR PRECURSOR
30810	6	N53419	Hs.47646	ESTs	
13348	6	AA449267	Hs.17914	ESTs	Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus]

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	CLUSTER	UNIGENE DESCRIPTOR
1789	6	L13258 AA036779 AA404282	Hs.936 Hs.61826 Hs.63481	Solute carrier family 17 (sodium phosphate) member 2 Homo sapiens clone 23928 mRNA sequence ESTs Weakly similar to kynurenine/alpha-aminoacidate aminotransferase [R.norvegicus]
16627	5			
27103	5			
12631	5	AA412293 AA242829 C01360 U53225	Hs.21258 Hs.7508 Hs.67364 Hs.75283	ESTs ESTs Homo sapiens clone 23904 mRNA sequence Sorting nexin 1
11599	5			
9010	5			
4660	5			
5244	5	U85992 AA284403 AA446114 D60419 AA456112 AA4562308 AA450127	Hs.87197 Hs.74750 Hs.55409 Hs.81915 Hs.99410 Hs.106385 Hs.110571	Human clone IMAGE:35527 unknown protein mRNA partial cds Homo sapiens mRNA for KIAA0554 protein partial cds ESTs STATMIN ESTs ESTs RESPONSE PROTEIN MYD118 [Mus musculus]
7953	5			
27617	5			
39480	5			
37529	5			
11858	5			
37294	5			
23201	5	T40652 D45608 M83652 H24456 AA425782 W68410 T80628 AA399271 AA460319 AFFX-	Hs.8279 Hs.83792 Hs.53155 Hs.85053 Hs.27973 Hs.106857 Hs.108169 Hs.19610 Hs.48469 AFFX-HLIMGAPDH/M33197_M	ESTs Surfactant pulmonary-associated protein D. Properdin P factor complement Homo sapiens clone 24440 mRNA sequence ESTs Calbindin 2 (29kD calretinin) ESTs ESTs ESTs ESTs
28767	5			
3151	4			
29196	4			
12863	4			
42486	4			
23571	4			
12376	4			
27894	4			
24935	4			

FIG.-6Ao

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	CLUSTER	UNIGENE DESCRIPTOR
4238	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds
41844	4	T15833	Hs.100227	EST
20111	4	N21380	Hs.25497	H.sapiens mRNA for ROX protein
8316	4	AA410529	Hs.30732	ESTs
39794	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)
9164	4	D38081	Hs.89887	Thromboxane A2 receptor
35027	4	AA349996	Hs.96937	ESTs
14158	4	AA490182	Hs.118598	ESTs
41950	4	T33137	Hs.7967	ESTs
34360	4	AA251547	Hs.104358	EST
6547	4	X95808	Hs.9568	Human mRNA for KIAA0385 gene complete cds
20863	4	N69989	Hs.19167	ESTs
12734	4	AA419200	Hs.5737	ESTs
39497	4	D80154	Hs.56340	ESTs
1600	4	K03474		EST - K03474
27148	4	AA406231	Hs.100113	Human mRNA for KIAA0381 gene partial cds
10763	4	AA057620	Hs.30807	ESTs
17007	4	AA069696	Hs.67317	ESTs
13522	4	AA454115	Hs.6000	ESTs
18444	4	AA232646	Hs.68061	ESTs
27665	3	AA447759	Hs.134724	PROTEIN KINASE C THETA TYPE
21382	3	R16896	Hs.89615	Inositol polyphosphate phosphatase-like protein 1 (51C protein)
2052	3	L36818	Hs.75339	ESTs
9039	3	C02049	Hs.106291	Human GT334 protein (GT334) gene mRNA complete cds
34888	3	AA303078	Hs.94479	

**FIG.-6Ap**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
11047	3	AA142849	Hs.22660	ESTs
19451	3	H23747	Hs.31697	ESTs
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I
13928	3	AA478441	Hs.11590	ESTs
12064	3	AA283848	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]
3836	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
4528	3	U48251	Hs.75871	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds
42064	3	T63364	Hs.9225	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parvimensis]
4596	3	U50743	Hs.19520	Sodium/potassium ATPase gamma subunit
4914	3	U67611		EST - U67611
20168	3	N24106	Hs.2799	Cartilage linking protein 1
24281	3	W79773	Hs.16511	ESTs
19634	3	H44866	Hs.31597	ESTs
10989	3	AA132366	Hs.8023	Homo sapiens mRNA for SPOP
6587	3	X97748		EST - X97748
14096	3	AA487558	Hs.8135	ESTs
13350	3	AA449297	Hs.8944	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]
33930	3	AA169539	Hs.95870	ESTs
34215	3	AA233855	Hs.104252	UTROPHIN
22509	3	R71393	Hs.29190	ESTs
20065	3	H98657	Hs.27291	ESTs
31091	3	N63076	Hs.138746	EST
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28913	3	F011560 AA598575	Hs.225583 Hs.12851	ESTs Highly similar to co-repressor protein [M.musculus] ESTs
14323	3	AA338729	Hs.133096	ESTs
34914	3	AA496891	Hs.5011	ESTs Weakly similar to The ha1237 gene product is related to S.pombe rad21 gene product. [H.sapiens]
14236	3	Z38804	Hs.22555	ESTs Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
24594	3	R79580 R52145 AA021284	Hs.29874 Hs.25894 Hs.60554	ESTs ESTs ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]
22589	3	H66642	Hs.88729	ESTs
22156	3	M26393	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain Probable transcription factor PML {alternative products}
16404	3	M79462	Hs.89633	ESTs
29310	3	H16568	Hs.23748	Human LIM protein MLP mRNA complete cds
9758	3	AA192614	Hs.83577	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
9806	2	W73790	Hs.73803	Nitric oxide synthase 3 (endothelial cell)
19289	2	M93718	Hs.769983	ESTs
34031	2	N75055	Hs.14632	ESTs
33299	2	R87373	Hs.75429	Protein kinase C substrate 80K-H
3276	2	R63695	Hs.1432	ESTs Weakly similar to No definition line found [C.elegans]
31704	2	N73988	Hs.37477	CDW52 antigen (CAMPATH-1 antigen)
10310	2	X62466	Hs.108338	ESTs Weakly similar to C06G8.3 [C.elegans]-
22388	2	R49689	Hs.5260	EST - RC_AA063316
20938	2	AA063316	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds
5935	2	AA464267		
41485	2			
25403	2			
27965	2			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
		ACCESSION	
40632	2	N45221	EST - RC_N45221
15527	2	W28798	Phosphodiesterase 6A cGMP-specific rod alpha
31672	2	N74336	ESTs
964	2	HG1804-	EST - HG1804-HT1829
12439	2	AA401452	ESTs
24223	2	W70158	ESTs
21052	2	N93764	ESTs Weakly similar to hypothetical protein [H.sapiens]
34140	2	AA215637	ESTs
5130	2	U79288	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Homo sapiens clone 24525 mRNA sequence
19202	2	H11509	ESTs
41350	2	R40442	Glutathione S-transferase M5
914	2	HG1019-	EST - HG1019-HT1019
31958	2	N93495	ESTs
12014	2	AA281769	Human Hpast (HPAST) mRNA complete cds
39777	2	H18412	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cos
19147	2	H09751	ESTs
11199	2	AA176446	ESTs
6477	2	X91504	Transcription factor COUP 2 (a.k.a. ARP1)
16336	2	AA018601	EXTRACELLULAR SIGNAL-REGULATED KINASE 3
24058	2	W23709	ESTs
26180	2	AA251230	ESTs
37177	2	AA447988	ESTs
41994	2	T47601	ESTs

**FIG.-6As**

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36532	2	AA429889	Hs.68882	Acrosin
1450	2	J03071	Hs.115352	Growth hormone 1
24819	2	Z40923	Hs.24812	ESTs
6532	2	X95325	Hs.89491	DNA-BINDING PROTEIN A
27085	2	AA402495	Hs.77978	ESTs
20487	2	N52322	Hs.19978	ESTs
724	2	D83703	Hs.30729	Peroxismal biogenesis factor 6
4132	2	U27655	Hs.82294	Human RGP3 mRNA complete cds
13375	2	AA449716	Hs.5723	ESTs
13988	2	AA480045	Hs.7934	ESTs
22306	2	R59906	Hs.100530	ESTs
23167	2	T33164	Hs.12840	Homo sapiens germline mRNA sequence
11320	2	AA213667	Hs.222222	ESTs
24608	2	Z38888	Hs.25046	ESTs
13163	2	AA437225	Hs.22410	ESTs
1139	2	HG3227-		EST - HG3227-HT3404
35572	2	AA401489		EST - RC_AA401489
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA
30963	2	N59373	Hs.26812	ESTs
16164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds
2174	2	L42611	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D
38958	2	AA609707	Hs.112751	ESTs
37919	2	AA478162	Hs.104965	ESTs
28905	2	D81123	Hs.57475	ESTs
3745	2	U09117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds
19545	2	H37834	Hs.32699	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
8416	2	AA428531		EST - AA428531
17569	2	AA128926		EST - RC_AA128926
19354	2	H18829	Hs.121515	ESTs
7598	2	AA174185	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds
25385	2	AA059099	Hs.109727	ESTs
14176	2	AA490620	Hs.11809	ESTs
29487	2	H85120	Hs.80881	N-ACETYL LACTOSAMINE SYNTHASE
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds
19488	2	H27675	Hs.25604	ESTs
10568	2	AA029703	Hs.36574	ESTs
30799	2	N53143	Hs.64001	ESTs
9638	2	L07592	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds
27195	2	AA411473	Hs.65311	ESTs
17438	2	AA115508	Hs.2780	Jun D proto-oncogene
24932	2	AFFX-AA07/X00351_M		AFFX-HS;AC07/X00351_M
10944	2	AA125969	Hs.34769	ESTs Weakly similar to F35G12.9 [C.elegans]
42324	2	T98199	Hs.142702	ESTs
34756	2	AA287665	Hs.8245	ESTs
12743	2	AA421050	Hs.24545	ESTs
13676	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2
13009	2	AA430474	Hs.16466	ESTs
7403	2	AA094921	Hs.79788	ESTs
35669	2	AA404707	Hs.54865	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17701	2	AA135941	Hs.71626	ESTs
18713	2	F04686	Hs.21782	ESTs
8314	2	AA410355	Hs.103081	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]
7990	2	AA291786	Hs.32822	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0168. [H.sapiens]
42791	2	AFFX-Z30643	Hs.123123	AFFX-HJMGAPDH/M33197_M
6893	1	AA402267	Hs.133475	H.sapiens mRNA for chloride channel (putative) 2139bp
35607	1	HA46074	Hs.31562	ESTs Weakly similar to zinc finger protein [H.sapiens]
9468	1	H82929		EST - RC_H82929
29469	1	F04444	Hs.6217	ESTs
18692	1	AA398161	Hs.97602	ESTs
35205	1	R53520	Hs.102755	ESTs
22184	1	D59267	Hs.56782	ESTs
28815	1	AA151480	Hs.91202	ESTs
17813	1	Z39191	Hs.27262	ESTs Weakly similar to Lph17p [S.cerevisiae]
24655	1	W51743	Hs.35096	ESTs
15611	1	W73859	Hs.78061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds
15700	1			EST - RC_AA435753
36770	1	AA435753	Hs.110783	ESTs
32400	1	R97176	Hs.20573	ESTs
10802	1	AA069425		EST - RC_AA129856
17593	1	AA129856	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]
20266	1	N32118		

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
14447	1	AA609045	Hs.11759	ESTs
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein
19738	1	H53059	Hs.15548	ESTs
14471	1	AA609346	Hs.20102	ESTs
5796	1	X55019	Hs.99975	Cholinergic receptor nicotinic delta polypeptide
18441	1	AA232508	Hs.77480	ESTs
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]
8830	1	AB002319	Hs.8663	Human rRNA for KIAA0321 gene partial cds
8682	1	AA477891	Hs.104476	ESTs
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]
35401	1	AA399593	Hs.97682	EST
10901	1	AA112307	Hs.25224	ESTs
19546	1	H37901	Hs.32706	ESTs
30292	1	N35978	Hs.82364	ESTs
39087	1	AA620607	Hs.111591	ESTs
37896	1	AA477463	Hs.77039	Ribosomal protein S28
41552	1	R59352	Hs.101253	Human rRNA for KIAA0296 gene complete cds
11467	1	AA234089	Hs.14593	ESTs
8215	1	AA389673	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]
15505	1	W28366	Hs.7252	Homo sajens clone 24800 mRNA sequence
9834	1	M92299	Hs.22554	Homeo box B5 (2.1 protein)
9159	1	D31483	Hs.90062	Homo sapiens clone 23565 unknown mRNA partial cds
42218	1	T86444	Hs.110095	ESTs
15526	1	W28790	Hs.8124	ESTs

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17790	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]
9777	1	M57888	Hs.95946	GRANZYME H PRECURSOR
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR
12076	1	AA284362	Hs.6448	ESTs Weakly similar to No definition line found [C.elegans]
15391	1	W26651	Hs.15961	ESTs
12905	1	AA427537	Hs.32419	ESTs
39820	1	H24085	Hs.25443	ESTs
13109	1	AA435838	Hs.7985	ESTs
24249	1	W73069	Hs.12600	ESTs
16514	1	AA027946	Hs.44608	ESTs
16767	1	AA046650	Hs.40342	ESTs
15381	1	W26496	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]
11690	1	AA252762	Hs.31235	ESTs
22999	1	T16510	Hs.6624	ESTs
24490	1	Z38153	Hs.26921	ESTs
24368	1	W87280	Hs.124800	ESTs
22565	1	R77631	Hs.29126	ESTs
15358	1	W26105	Hs.8961	ESTs
24186	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]
22272	1	R58922	Hs.26590	ESTs
16434	1	AA024494	Hs.61199	ESTs
22692	1	R88711	Hs.34183	ESTs
38830	1	AA609189	Hs.116415	ESTs
42547	1	W73946	EST - RC_W73946	Homo sapiens p38beta2 MAP kinase mRNA complete cds
34885	1	AA302831	Hs.57732	

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18445	1	AA232648	Hs.87068	ESTs
18070	1	AA180352	Hs.72733	ESTs
23923	1	T96407	Hs.17812	ESTs

*FIG.-6Ay*

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74126	H.sapiens mRNA for I-15P (I-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M19828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-II/urolguanylin precursor
1304	>10	HG4310		EST - H34310-HT4580
5980	>10	X64559	Hs.65424	Ttranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase)
24461	>10	W94427	Hs.3807	congenital adrenal hyperplasia)
				ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING
				ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.28264	ESTs
41148	>10	R06984		EST - RC_R06984_s
31652	>10	N73958	Hs.50404	Human chemokine (T ECK) mRNA complete cds
23483	>10	T68873	Hs.143289	H.sapiens mRNA for metallothionein isoform_1R
4605	>10	U51010		EST - U51010
28359	>10	AA609133	Hs.58115	ESTs

FIG.-7Aa

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N64436	Hs.20813	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403032	Hs.21701	ESTs
42059	>10	T61654	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
25468	>10	AA079072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs
16938	>10	AA059473	Hs.66783	ESTs
41788	>10	T03735	Hs.26885	ESTs
7754	>10	AA234634	Hs.76722	Human NF-IL6-beta protein mRNA complete cds
6122	>10	X72012	Hs.75962	Endoglin (Osler-Rendu-Weber syndrome 1)
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
23013	>10	T16661	Hs.6725	ESTs
19537	>10	H30270	Hs.32583	ESTs
4584	>10	U50360	EST - U50360	EST
37410	>10	AA453652	Hs.99344	ESTs
27969	>10	AA464594	Hs.63382	ESTs
35497	>10	AA400606	Hs.144344	EST

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37013	>10	AA443690	Hs.136268	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens] ESTs
39247	>10	AA621553	Hs.112998	
13471	>10	AA452598	Hs.109590	
42110	>10	T68878	Hs.76688	Carboxylesterase 2 (liver)
10965	>10	AA128997	Hs.18953	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds
49118	>10	U67733	Hs.3831	Human cGMP-stimulated 3'5'-cyclic nucleotide phosphodiesterase PDE2A5 (PDE2A) mRNA complete cds H.sapiens KHK mRNA for ketohexokinase clone pHKH3a
40737	>10	N54950	Hs.81454	
30403	>10	N45300	Hs.110647	
11432	>10	AA233369	Hs.361	
18784	>10	F09748	Hs.7974	
40662	>10	N49281		EST - RC_N49281
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1
35041	>10	AA350586	Hs.30862	ESTs
20868	>10	N70068	Hs.7243	ESTs
39729	>10	H11489	Hs.105805	ESTs
27387	>10	AA426330	Hs.78264	ESTs
39758	>10	H15814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds
43119	>10	U37283	Hs.58882	Human microfibril-associated glycoprotein-2 MAGP-2 mRNA complete cds
2866	>10	M59815	Hs.76682	
30332	>10	N39075	Hs.44934	Complement component 4A EST
41344	>10	R40189	Hs.6985	ESTs

**FIG.-7Ac**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28271	>10	AA521200	Hs.48778	ESTs
5834	>10	X57129	Hs.7644	HISTONE H1D
19048	>10	H05464	Hs.100251	ESTs
1429	>10	J02854	Hs.9615	Human 2.0-kDa myosin light chain (MLC-2) mRNA complete cds
19491	>10	H27910	Hs.107384	ESTs
29992	>10	N26386	Hs.33084	Solute carrier family 2 (facilitated glucose transporter) member 5
2041	>10	L36033	Hs.77423	Stromal cell-derived factor 1
22865	>10	R99909	Hs.36186	ESTs
11624	>10	AA243654	Hs.17998	ESTs
12512	>10	AA405199	Hs.20733	ESTs
41443	>10	R45577	Hs.10683	ESTs
5055	>10	U77180	Hs.50002	Human mRNA for EBI1-ligand chemokine complete cds
6038	>10	X66945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)
42530	>10	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds
37350	>10	AA452606	Hs.99289	EST
37488	>10	AA455178	Hs.99397	ESTs
36646	>10	AA431797	Hs.98763	EST
38999	>10	AA609907		EST - RC_AA609907
38191	>10	AA487895	Hs.17311	ESTs
9944	>10	N57464	Hs.74670	Human mRNA for KIAA0146 gene partial cds
8139	>10	AA341723	Hs.107374	ESTs
41522	>10	R53966	Hs.75092	N-CHIMERAERIN

FIG.-7Ad

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38900	>10	AA482603	Hs.111301	Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)
41175	>10	R09241	EST - RC_R09241	
36947	>10	AA437388	Hs.115726	ESTs
4175	>10	U29953	Hs.76110	Pigment epithelium-derived factor
35421	>10	AA399686	Hs.97669	EST
4358	>10	U39487	Hs.250	Xanthine dehydrogenase
35463	>10	AA400272	Hs.97758	EST
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
34625	>10	AA282238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds
20179	>10	N24879	Hs.9693	ESTs
36805	>10	AA435901	Hs.56874	ESTs Weakly similar to p20 protein [R.norvegicus]
24447	>10	W93121	Hs.23841	Human mRNA for KIAA0355 gene complete cds
10247	>10	R74386	Hs.108924	ESTs
3618	>10	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF)
		F08876	Hs.8008	ESTs
		R73075	Hs.29327	EST
		AA455960	Hs.99405	ESTs
		R05483	Hs.138500	ESTs
		U42031	Hs.7557	Human 54 kDa progesterone receptor-associated immunophilin FKBP54 mRNA partial cds
		M14777	Hs.89552	Glutathione S-transferase A2
18730	>10	AA421142	Hs.104672	ESTs
22529	>10	U43653	Hs.3261	Leptin (mammalian obesity homolog)
37520	>10	H53728	Hs.36808	ESTs
41122	>10			
4417	>10			
9742	>10			
36194	>10			
4445	>10			
19749	>10			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19793	>10	H56965	Hs.34564	ESTs
12713	>10	AA418398	Hs.17778	ESTs
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR
16842	>10	AA055163	Hs.57975	Homo sapiens mRNA for cardiac calsequestrin complete cds
34229	>10	AA234383	Hs.3576	ESTs
35563	>10	AA401404	Hs.112087	ESTs
16736	>10	AA045306	Hs.42996	ESTs
33607	>10	W93497	Hs.59486	ESTs
16146	>10	AA005236	Hs.60162	ESTs
22666	>10	R85880	Hs.33455	ESTs
22562	>10	R77493	Hs.29653	EST
22985	>10	T16211	Hs.6326	Homo sapiens clone 23798 and 23825 mRNA sequence
5248	>10	U86358	Hs.50404	Human chemokine (TECK) mRNA complete cds
27608	>10	AA443800	Hs.43125	ESTs
7510	>10	AA136353	Hs.38022	ESTs
34683	>10	AA284920	Hs.13716	ESTs
27633	>10	AA446659	Hs.2563	Tachykinin 2 (substance K neurokinin A neurokinin 2 neuromedin L neurokinin alpha neuropeptide K neuropeptide gamma)
32485	>10	T16335	Hs.65325	EST
38791	>10	AA609018	Hs.112629	ESTs
32020	>10	N95796	Hs.55181	ESTs
19986	>10	H89980	Hs.12112	Moderately similar to protein phosphatase 1 binding protein PTG [M.rnuscus]
30748	>10	N52254	Hs.47438	ESTs
8903	>10	AF002246	Hs.21226	Homo sapiens neural cell adhesion molecule (CALL) mRNA complete cds

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
9959	>10	N75215	Hs.43148	ESTs
38136	>10	AA486185	Hs.125176	ESTs
19845	>10	H59887	Hs.35167	ESTs
1127	>10	HG3117-	EST - HG3117-HT3293	
23637	>10	T85315	Hs.15903	ESTs
16699	>10	AA043349	Hs.62630	ESTs
36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
28930	>10	F02702	Hs.141503	Small incducible cytokine A5 (RANTES)
9226	>10	D62584	Hs.109439	ESTs Highly similar to OSTEOINDUCTIVE FACTOR PRECURFISOR [Bos taurus]
3357	>10	M99487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36783	>10	AA435805	Hs.112065	EST
4876	>10	U66061	Hs.2048	Protease serine 2 (trypsin 2)
41149	>10	R06986	Hs.76487	ESTs
22200	>10	R54179	Hs.26100	ESTs
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin
10911	>10	AA113387	Hs.24305	ESTs
3336	>10	M97675	Hs.1944	Human protein tyrosine kinase t-Ror1 (Ror1) mRNA complete cds
31889	>10	N91897	Hs.50652	ESTs
10406	>10	AA007629	Hs.25478	ESTs
17737	>10	AA142875	Hs.71719	ESTs
38939	>10	AA609632	Hs.112737	EST
16206	>10	AA010611	Hs.60418	EST
32810	>10	W15376	Hs.122656	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18210	>10	AA196306	Hs.86045	ESTs
24054	>10	W15580	Hs.15342	ESTs
23047	>10	T23457	Hs.7120	ESTs
12944	>10	AA428258	Hs.8769	ESTs
341172	>10	AA227469	Hs.139171	EST
9317	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
19331	>10	H177865	Hs.23213	ESTs
21035	>10	N92824	Hs.14898	ESTs
34208	>10	AA233380	Hs.104249	Integrin beta 2 (antigen CD18 (p95) lymphocyte function-associated antigen 1 macrophage antigen 1 (mac-1) beta subunit)
5974	>10	X64072	Hs.83968	associated antigen 1 macrophage antigen 1 (mac-1) beta subunit (TRF1) mRNA
5032	>10	U74382	Hs.90357	Homo sapiens telomeric repeat binding factor p20 (RPP20) complete cds
41941	>10	T32561	Hs.5476	ESTs
34239	>10	AA235009	Hs.32246	ESTs
32852	>10	W31906	Hs.116428	ESTs
7662	>10	AA203527	Hs.18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
6432	>10	X89066	Hs.94413	Transien receptor potential channel 1
37001	>10	AA443311	Hs.98998	ESTs
4630	>10	U52101	Hs.9999	Human YMP mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs
28483	>10	C14270	Hs.66357	ESTs
19801	>10	H57357	Hs.18767	ESTs Weakly similar to unknown protein [H.sapiens]
24672	>10	Z39300	Hs.124952	ESTs
31153	>10	N63688	EST - RC_N63688	

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40250	>10	H92451	Hs.110	Solute carrier family 3 (cystine dibasic and neutral amino acid transporters activator of cystine dibasic and neutral amino acid transport) mem
23028	>10	T177215	Hs.6952	ESTs
28072	>10	AA480886	Hs.86693	ESTs
11868	>10	AA262556	Hs.28802	ESTs Weakly similar to centaurin alpha [R.norvegicus]
35359	>10	AA399061	Hs.112961	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4285	>10	U35139	Hs.50130	Human NECDIN related protein mRNA complete cds
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235984	Hs.87469	ESTs
2042	>10	L36051	Hs.1166	Thrombopoletin (myeloproliferative leukemia virus oncogene ligand megakaryocyte growth and development factor)
25262	>10	AA043501	Hs.30250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds
34821	>10	AA291983	Hs.144599	ESTs
42405	>10	W44682	Hs.109896	ESTs
41348	>10	R40395	Hs.112125	Lecithin- $\alpha$ -cholesterol acyltransferase
14494	>10	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	>10	U43916	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
2098	>10	L39009	EST - L39009	
35637	>10	AA402933	Hs.29283	ESTs
16549	>10	AA029697	Hs.94854	ESTs
1220	>10	HG3733-	EST- HG3733-HT4003	

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PRIMARY KEY	FOLD OF TUMOR vs.	DOWNSREGULATED	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39934	>10		H52185	Hs.124994	ESTs
7735	>10		AA232121	Hs.109631	Human tyrosyl-tRNA synthetase mRNA complete cds
40392	>10		H99587	Hs.108880	ESTs
37170	>10		AA447779	Hs.991145	EST
18361	>10		AA223902	Hs.86899	ESTs
19366	>10		H19204	Hs.133466	ESTs
38429	>10		AA496965	Hs.108694	Glycophorin A
38021	>10		AA481059	Hs.105152	ESTs
5184	>10		U82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
27863	>10		AA458923	Hs.70202	ESTs Weakly similar to F23B2.4 [C.elegans]
37476	>10		AA455051	Hs.99386	EST
859	>10		D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
27185	>10		AA410895	Hs.62348	ESTs
41010	>10		N80686	Hs.21639	Human APEG-1 mRNA complete cds
38241	>10		AA489076	Hs.105101	ESTs
22701	>10		R89477	Hs.34299	ESTs
12152	>10		AA291271	Hs.10886	ESTs Weakly similar to uroporphyrinogen III synthase UROIII S [H.sapiens]
			AA609531	Hs.112050	ESTs
			AA192871	Hs.83760	Tropomin I (skeletal fast)
			AA459857	Hs.99503	EST
			U29725	Hs.3080	Human EiMK1 alpha kinase mRNA complete cds
			AA009839	Hs.1632	CD27L RECEPTOR PRECURSOR
			N54161	Hs.124044	ESTs
			T25873	Hs.102243	ESTs
38913	>10				
34034	>10				
37644	>10				
4173	>10				
16178	>10				
20527	>10				
41918	>10				

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
1525	>10	J04621	Hs.1501	Syndecan 2 (heparan sulfate proteoglycan 1 cell surface-associated fibroglycan)
19160	>10	H10208	Hs.30972	EST
16860	>10	AA055833	Hs.58152	ESTs Weakly similar to Natsu [M.musculus]
36927	>10	AA437259	Hs.104944	EST
1595	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.26216	ESTs
8985	>10	C00125	Hs.24332	ESTs Weakly similar to similar to deoxyribose-phosphate aldolase [C.elegans]
33995	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds
7949	>10	AA283620	Hs.34956	ESTs
16607	>10	AA034918	Hs.85079	ESTs
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
7354	>10	AA092348	Hs.7858	ESTs
4277	>10	U34879	Hs.85279	ESTRADIOL 17 BETA-DEHYDROGENASE 1
23214	>10	T40895	Hs.11937	Human protein tyrosine phosphatase-PTPCAAX1 (hPTPCAAX1) mRNA complete cds
22209	>10	R54594	Hs.25209	ESTs
36151	>10	AA419011	Hs.96744	ESTs
23372	>10	T59537		EST - RC: T59537
42136	>10	T72491	Hs.73849	Apolipoprotein C-III
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit
15974	>10	Z36531	Hs.2659	H.sapiens mRNA for fibrinogen-like protein (pT49 protein)
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0673 protein partial cds

**FIG.-7AK**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34764	>10	AA287870	Hs.890	Lymphotoxin-beta
24027	>10	W01875	Hs.5734	Homo sapiens mRNA for KIAA0679 protein partial cds ESTs
36197	>10	AA421158	Hs.97514	EST - RC_AA448334
37211	>10	AA448334		ESTs
27684	>10	AA448625	Hs.57929	ESTs
31790	>10	N80279	Hs.50891	ESTs
24515	>10	Z38289	Hs.12701	ESTs
18652	>10	F03111	Hs.22505	ESTs
16635	>10	AA037433	Hs.46987	ESTs
37815	>10	AA469952	Hs.97899	Prostaglandin E receptor 3 (subtype EP3) {alternative products}
6364	>10	X83857	Hs.495	ESTs Weakly similar to !!! ALU SUBFAMILY SX WARNING
9034	>10	C01833	Hs.29759	ENTRY !!! [H.sapiens]
16469	>10	AA025728	Hs.61307	ESTs
27034	>10	AA400102	Hs.49051	ESTs
42746	>10	Z40646	Hs.124953	ESTs
35368	>10	AA399269	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds
34805	>10	AA291522	Hs.97250	EST
19983	>10	H89355	Hs.6598	ESTs
31126	>10	NG3444	Hs.47566	ESTs
22616	>10	R81949	Hs.124964	ESTs
12246	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (hGB1a) receptor
8777	>10	AA495865	Hs.7974	ESTs
13486	>10	AA453034	Hs.21041	ESTs Highly similar to FIBROPELLIN C PRECURSOR [Strongylacentrotus purpuratus]
25512	>10	AA085721	Hs.95511	ESTs

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
29073	>10	F12567		EST - RC_F12567
5541	>10	X07203	Hs.89751	CD20 RECEPTOR
41689	>10	R82942	Hs.107755	ESTs Weakly similar to GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE [E.coli]
32343	>10	R80965	Hs.125052	ESTs
38335	>10	AA490916	Hs.112157	ESTs
41729	>10	R92458	Hs.89554	Hemoglobin gamma-G
36707	>10	AA434246	Hs.98802	EST
28491	>10	C14784	Hs.12382	ESTs
41702	>10	R86970	Hs.123363	ESTs
32246	>10	R52163	Hs.144526	ESTs
17314	>10	AA086487	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]
30325	>10	N38967	Hs.44904	EST
19823	>10	H58692	Hs.9520	ESTs Highly similar to FORMYL-TETRAHYDROFOLATE DEHYDROGENASE [Rattus norvegicus]
42153	>10	T77729	Hs.89890	Pyruvate carboxylase
19321	>10	H17511	Hs.24963	ESTs
27110	>10	AA404494	Hs.84112	CTP synthetase
28831	>10	D59722	Hs.92924	ESTs
6333	>10	X82494	Hs.2653	Fibulin 2
37679	>10	AA460661	Hs.99562	ESTs
40829	>10	N64344	Hs.78362	Human clone 23839 mRNA sequence
19132	>10	H09343	Hs.27261	ESTs
19353	>10	H18706	Hs.31604	ESTs
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]

FIG.-7Am

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
11621	>10	AA243574	Hs.14691	ESTs
38538	>10	AA521370	Hs.104423	ESTs
10095	>10	R22139	Hs.30343	ESTs
30014	>10	N26740	Hs.42771	ESTs
4464	>10	U44429	Hs.16611	Human D53 (hD53) mRNA partial cds
3650	>10	U03877	Hs.76224	Human extracellular protein (S1-5) mRNA complete cds
36377	>10	AA426056	Hs.98450	ESTs
20437	>10	N50550	Hs.24587	Homo sapiens mRNA for Eif1 complete cds
1576	>10	K02100	Hs.117050	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR
42078	>10	T64891	Hs.144323	ESTs
27257	>10	AA418001	Hs.46146	ESTs Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]
30582	>10	N49848	Hs.46974	EST
3631	>10	U03090	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds
19026	>10	H04768	Hs.30484	ESTs
4752	>10	U59632	Hs.3847	Glycoprotein Ib (platelet) beta polypeptide
3766	>10	U09579	Hs.74984	CYCLIN-DEPENDENT KINASE INHIBITOR 1
1437	>10	J02923	Hs.76506	Lymphocyte cytosolic protein 1 (L-plastin)
33905	>10	AFFX-TmX-5		AFFX-TmX-5
4310	>10	U37055	Hs.76034	Macrophage stimulating 1 (hepatocyte growth factor-like)
26923	>10	AA342302	Hs.55036	ESTs
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
37571	>10	AA457409	Hs.99458	EST
38800	>10	AA609052	Hs.112636	EST
27952	>10	AA463700	Hs.47042	Homo sapiens CD39L3 (CD39L3) mRNA complete cds

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27621	>10	AA446242	Hs.56589	ESTs Testis specific protein Y-linked-
38784	>10	AA608988	Hs.2051	
291	>10	D16532	Hs.73729	Very low density lipoprotein receptor
18014	>10	AA173168	Hs.57672	ESTs Weakly similar to weakly similar to myosin heavy chain [C.elegans]
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
39953	>10	H56010	Hs.108144	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
13777	>10	AA463504	Hs.6052	ESTs
13419	>10	AA450336	Hs.22269	ESTs
1403	>10	J00123	Hs.93557	PROENKEPHALIN A PRECURSOR
42373	>10	W35362	Hs.103012	ESTs
21520	>10	R28267	Hs.24258	ESTs
9796	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
35650	>10	AA404271	Hs.22631	Human glutamate receptor (GLUR5) mRNA complete cds
42501	>10	W69586	Hs.103156	ESTs
33812	>10	Z41239	Hs.106960	ESTs
42473	>10	W63731	Hs.122531	ESTs
25195	>10	AA033790	Hs.75736	Apolipoprotein D
28607	>10	C21481	Hs.84630	ESTs Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]
3712	>10	U07620	Hs.89661	Human MAP kinase mRNA complete cds
6214	>10	X77307	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23575	>10	T80833	Hs.14794	ESTs
31775	>10	N79765	Hs.50847	ESTs
5206	>10	U82979	Hs.67846	Human clone HM18 monocyte inhibitory receptor precursor mRNA complete cds
22769	>10	R94521	Hs.124693	ESTs
9377	>10	H12674	Hs.9396	ESTs
29268	>10	H61046	Hs.70405	EST Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
11061	>10	AA147537	Hs.4811	ESTs
41960	>10	T33511	Hs.4844	ESTs
29416	>10	H77734	Hs.36702	Homo sapiens roundabout 1 (robo1) mRNA complete cds
38248	>10	AA489218	Hs.105229	ESTs
37256	>10	AA449424	Hs.98428	ESTs
21911	>10	R43980	Hs.26320	ESTs
23184	>10	T34622	Hs.8108	ESTs Weakly similar to HYPOTHETICAL 35.8 KD PROTEIN IN PRP13-SRP40 INTERGENIC REGION [S.cerevisiae]
16225	>10	AA011305	Hs.10029	Cathepsin C
27766	>10	AA453656	Hs.88417	ESTs
16071	>10	AA001426	Hs.40863	ESTs
17343	>10	AA100152	Hs.5921	ESTs
10643	>10	AA040154	Hs.32478	ESTs
29335	>10	H6B239	Hs.39122	ESTs
34966	>10	AA344866	Hs.1285	Complement component 8 gamma polypeptide
26303	>10	AA255483	Hs.88042	EST
1030	>10	HG2416-	EST - HG2416-HT2512	
28370	>10	AA609559	Hs.38550	ESTs Moderately similar to alfa subunit [H.sapiens]

**FIG.-7A**

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
29303	>10	H65881	Hs.38427	ESTs
21076	>10	N99976	Hs.8016	ESTs
27100	>10	AA404231		EST - RC_AA404231
11329	>10	AA216589	Hs.28462	ESTs
4402	>10	U41518	Hs.74602	AQUAPORIN-CHIP
11050	>10	AA142919	Hs.5558	ESTs
22844	>10	R98947		EST - RC_R98947
31581	>10	N71371	Hs.39938	ESTs
7253	>10	AA074407	Hs.139119	ESTs
20423	>10	N49308	Hs.104938	ESTs
39264	>10	AA621750		EST - RC_AA621750
36415	>10	AA426598	Hs.24897	Homo sapiens chromosome 21q22.1 anonymous mRNA sequence!
16575	>10	AA031948	Hs.57548	ESTs
37505	>10	AA455659	Hs.103233	ESTs
28264	>10	AA521080	Hs.46765	ESTs
23886	>10	T95325	Hs.16545	ESTs
11781	>10	AA256485	Hs.33413	ESTs
25603	>10	AA114250	Hs.48924	Homo sapiens mRNA for KIAA0512 protein complete cds
9003	>10	C00808	Hs.107882	ESTs
5632	>10	X15357		EST - X15357
7680	>10	AA206946	Hs.8059	ESTs
22783	>10	R95689	Hs.35437	ESTs
20852	>10	N69540	Hs.17713	ESTs
16795	>10	AA047896	Hs.49169	ESTs
37558	>10	AA456975	Hs.75736	Apolipoprotein D

**FIG.-7Aa**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
35957	>10	AA412537	Hs.98149	EST
42129	>10	T71561	Hs.84824	ESTs
34585	>10	AA281002	Hs.40735	ESTs
33690	>10	Z38607	Hs.62248	ESTs
8904	>10	AF002256	Hs.86180	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds
2689	>10	M32373	Hs.1256	Arylsulfatase B
40909	>10	N69084	Hs.49608	ESTs
22377	>10	R63090	Hs.28391	ESTs
21208	>10	R07651	Hs.20023	EST
27304	>10	AA4421783	Hs.56808	Homo sapiens mRNA for zinc finger protein FPM315 complete cds
3307	>10	M95809	Hs.89578	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT
25370	>10	AA057556	Hs.28478	ESTs
41423	>10	R44717	Hs.22917	ESTs
2570	>10	M27160	Hs.2053	Tyrosinase (oculocutaneous albinism IA)
14557	>10	AA620965	Hs.108300	ESTs Highly similar to ADENYLOSUCCINATE SYNTHETASE MUSCLE ISOZYME [Mus musculus]
7023	>10	Z78291		EST - Z78291
31051	>10	N62696	Hs.48607	EST
39200	>10	AA621246	Hs.112956	EST
24712	>10	Z39652	Hs.27457	ESTs
23296	>10	T52497	Hs.9444	ESTs Moderately similar to !!! ALU CLASS A WARNING ENTRY !!! [H.sapiens]
12826	>10	AA4424806	Hs.134646	ESTs
2199	>10	L49169	Hs.75678	Human C0S3 mRNA complete cds

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27226	>10	AA416767	Hs.43498	ESTs
7135	>10	AA028976	Hs.8175	ESTs
17102	>10	AA074955		EST - RC_AA074955
38942	>10	AA609646	Hs.94970	Human mRNA for KIAA0306 gene partial cds
29288	>10	H64973	Hs.38336	ESTs
34336	>10	AA250843	Hs.54434	Interferon regulatory factor 5
30816	>10	N53566	Hs.47681	ESTs
16739	>10	AA045461	Hs.65093	ESTs
42317	>10	T97599	Hs.113025	ESTs
2228	>10	L77563		EST - L77563
30862	>10	N55171	Hs.47927	ESTs
35954	>10	AA412526	Hs.97951	ESTs
36403	>10	AA426383	Hs.98467	ESTs
36949	>10	AA441812	Hs.98959	ESTs
41628	>10	R70212	Hs.79630	Immunoglobulin-associated alpha
39175	>10	AA621076	Hs.111996	ESTs
37657	>10	AA460147	Hs.98397	EST - RC_AA460147
36279	>10	AA424242		protein [M.musculus]
6834	>10	Z18954	Hs.2960	S100 calcium-binding protein A5 (formerly S100D)
40562	>10	N33212	Hs.107197	ESTs
13770	>10	AA463272	Hs.22636	ESTs
5101	>10	U79249	Hs.78362	Human clone 23839 mRNA sequence
3355	>10	M99438	Hs.31305	Human transducin-like enhancer protein (TLE3) mRNA complete cds
8476	>10	AA442119	Hs.29790	ESTs
				<b>FIG.-7As</b>

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34231	>10	AA234527	Hs.75772	Glucocorticoid receptor
42046	>10	T59148	Hs.50966	Carbamoyl-phosphate synthetase 1 mitochondrial ESTs
23913	>10	T96123	Hs.17749	TRANSFORMING PROTEIN RHOB ESTs
37333	>10	AA452158	Hs.75122	
27946	>10	AA463434	Hs.42658	
34407	>10	AA255523	EST - RC_AA255523	
16542	>10	AA029428	Hs.61555	ESTs
6248	>10	X78712	Hs.98008	Glycerol kinase 2 (testis specific)
8227	>10	AA393666	Hs.75709	Mannose-6-phosphate receptor (cation dependent) EST - S78774
3507	>10	S78774		ESTs
40907	>10	N68830	Hs.25717	ESTs
33340	>10	W779698	Hs.58550	ESTs
19079	>10	H06371	Hs.20945	ESTs
3992	>10	U19713	Hs.76364	Allograft inflammatory factor 1 ESTs
36059	>10	AA417063	Hs.98189	EST
37634	>10	AA459662	Hs.99489	EST
41581	>10	R62313	Hs.126270	ESTs Weakly similar to RTP60 [R.norvegicus]
38734	>10	AA608792	Hs.112591	EST
37836	>10	AA470135	Hs.112238	ESTs
21303	>10	R11157	Hs.12610	ESTs
20125	>10	N22006	Hs.6202	ESTs
35516	>10	AA400795	Hs.97450	ESTs
26771	>10	AA284067	Hs.89267	EST
33558	>10	W90735	Hs.59332	EST
2830	>10	M57399	Hs.44	Pleiotrophin (heparin binding growth factor 8 neurite growth-promoting factor 1)

**FIG.-7At**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42625	>10	W88426	Hs.110128	ESTs
26152	>10	AA250845	Hs.87762	ESTs
31988	>10	N94581	Hs.55062	ESTs
17763	>10	AA148213	Hs.71873	ESTs Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]
21959	>10	R44949	Hs.22906	ESTs
10000	>10	N79674	Hs.7915	ESTs
30658	>10	N51105	Hs.111223	ESTs
17629	>10	AA131919	Hs.69009	ESTs
36260	>10	AA423970	Hs.98378	ESTs
285	>10	D16227	Hs.3618	Hippocalcin-like 1
26123	>10	AA243598	Hs.20887	ESTs
34535	>10	AA279391	Hs.104425	EST
29100	>10	H01428	Hs.92350	ESTs
24122	>10	W46947	Hs.4188	ESTs
19894	>10	H65942	Hs.36030	ESTs
22987	>10	T16258	Hs.25420	ESTs
5985	>10	X64728	Hs.34514	H.sapiens CHML mRNA
42461	>10	W60008	Hs.89717	Human preprocarboxypeptidase A2 (proCPA2) mRNA complete cds
5422	>10	X00588	Hs.77432	Epidermal growth factor receptor
16603	>10	AA034366	Hs.144627	ESTs
33389	>10	W81607	Hs.58663	EST
6931	>10	Z46788	Hs.3232	H.sapiens mRNA for cyclin II
19324	>10	H17618	Hs.28180	ESTs
32166	>10	R41836	Hs.9657	ESTs

**FIG.-7Au**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39967	>10	H58415	Hs.102160	EST
17958	>10	AA166917	Hs.72639	ESTs Highly similar to MITOCHONDRIAL RESPIRATORY
38569	>10	AA598437	Hs.29385	CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 [Saccharomyces cereisia
1006	>10	HG2260-T79638	Hs.105618	ESTs
23552	>10	AA488997	Hs.137530	ESTs
38228	>10	HG2705-T91283		EST - HG2705-HT2801
1066	>10	U57099	Hs.21639	EST - RC_T91283
23815	>10	N66796	Hs.144212	Human AP EG-1 mRNA complete cds
4699	>10	AA399633	Hs.24872	ESTs
31306	>10	AA279662	Hs.142462	ESTs Moderately similar to snRNP protein B [H.sapiens]
12389	>10	N39584	Hs.17404	ESTs
34539	>10	AA236868	Hs.87564	ESTs
20358	>10	AA488659	Hs.105686	ESTs
26070	>10	AA235874	Hs.888888	PUTATIVE DNA BINDING PROTEIN A20
38210	>10	U71207	Hs.29279	Homo sapiens clone 24534 eyes absent homolog (Eab1) mRNA partial cds
26025	>10	U68162	Hs.84171	THROMBOPOEITIN RECEPTOR PRECURSOR
4978	>10	S78467		EST - S78467
4935	>10	AA505136	Hs.12420	ESTs
3501	>10	N90688	Hs.54643	EST
14281	>10	R01398		EST - RC_R01398
31859	>10			
41104	>10			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
		ACCESSION	
5293	>10	U89995	Hs.95206 Human DNA binding protein FKHL15 (FKHL15) mRNA complete cds EST - S81957
3543	>10	S81957	ESTs
27615	>10	AA443958	Hs.90960 Homo sapiens mRNA for KIAA0525 protein partial cds ESTs
7152	>10	AA036753	Hs.78494 Homo sapiens mRNA for KIAA0525 protein partial cds ESTs
16197	>10	AA010328	Hs.39379 Homo sapiens putative transmembrane protein (CLN5) mRNA complete cds
20176	>10	N24772	Hs.30213 Homo sapiens putative transmembrane protein (CLN5) mRNA complete cds
33586	>10	W93015	Treacher Collins syndrome susceptibility protein ESTs
27265	>10	AA418392	Hs.46784 ESTs
12453	>10	AA402000	Hs.20415 Weakly similar to GS3786 [H.sapiens] ESTs
36302	>10	AA424652	Hs.124985 ESTs
23192	>10	T40448	Hs.8204 ESTs
17423	>10	AA114071	Hs.26270 ESTs
23464	>10	T67026	Hs.13019 ESTs
42762	>10	Z41697	Hs.106296 ESTs
32628	>10	T56470	Hs.119190 Chromogranin A (parathyroid secretory protein 1) ESTs
12805	>10	AA424331	Hs.29640 Human adenylyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds
25379	>10	AA058893	Hs.111841 Homo sapiens mRNA for KIAA0515 protein partial cds ESTs
39318	>10	C20617	Hs.108945 Glucocorticoid receptor ESTs
29699	>10	H97938	Hs.75772 ESTs
17907	>10	AA160530	Hs.72447 ESTs
35819	>10	AA411011	Hs.8038 Homo sapiens Pig12 (PIG12) mRNA complete cds ESTs
36838	>10	AA436163	Hs.95851 ESTs
29611	>10	H94043	Hs.41949 ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19650	>10	H46167	Hs.31542	ESTs
33221	>10	W70305	Hs.64859	ESTs
18840	>10	F10265	Hs.13287	ESTs
2580	>10	M27533		EST - ME7533
7274	>10	AA082171	Hs.8261	ESTs
19524	>10	H29566	Hs.83466	Homo sajiens clone 23579 mRNA sequence
40571	>10	N33558	Hs.103102	ESTs Weakly similar to WWP2 [H.sapiens]
31178	>10	N64191	Hs.46584	ESTs
29894	>10	N23009	Hs.43296	ESTs
22201	>10	R54416	Hs.140932	ESTs
26719	>10	AA282583	Hs.88617	ESTs
32493	>10	T16497	Hs.65339	EST
37179	>10	AA448004	Hs.99150	ESTs
17980	>10	AA169173	Hs.72754	ESTs
21934	>10	R44449	Hs.48778	ESTs
36792	>10	AA435848		EST - RC_AA435848
34056	>10	AA194851	Hs.110575	ESTs
39102	>10	AA620674	Hs.112882	EST
26283	>10	AA253217	Hs.41271	ESTs
23989	>10	T98529	Hs.18398	ESTs
32456	>10	T15829	Hs.65264	ESTs
15440	>10	W27301	Hs.111652	Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonospora curvata]
19004	>10	H03299	Hs.30390	EST
27839	>10	AA456309	Hs.58831	ESTs
18848	>10	F10338	Hs.106309	Moderately similar to FOG [M.musculus]

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
13112	>10	AA435896	Hs.18397	ESTs
1850	>10	L17325	Hs.278	Human pre-T/NK cell associated protein (1D12A2) mRNA complete cds
9101	>10	C17938	Hs.25536	ESTs
2807	>10	M55210	Hs.87428	Laminin gamma 1 (formerly LAMB2)
3383	>10	S57153	Hs.91797	Retinoblastoma-binding protein 1 {alternative products}
23142	>10	T26444	Hs.101248	ESTs
5367	>10	U95019	Hs.30941	Myasthenic syndrome antigen B [human fetal brain mRNA 3477 nt]
32205	>10	R44234	Hs.75169	ESTs
26515	>10	AA262972	Hs.87298	ESTs
15332	>10	W24127	Hs.16003	ESTs Weakly similar to keratin 8 type II cytoskeletal embryonic [M.musculus]
34193	>10	AA232251	Hs.128630	ESTs
6392	>10	X85753	Hs.25283	CELL DIVISION PROTEIN KINASE 8
33784	>10	Z40689	Hs.65973	ESTs
33474	>10	W87484	Hs.50429	ESTs
34964	>10	AA344854	Hs.96837	ESTs
14584	>10	AA621414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
22640	>10	R83664	Hs.33416	EST
4339	>10	U38372	EST - U33372	EST - U33372
37557	>10	AA456966	Hs.41548	Human MHC Class I region proline rich protein mRNA complete cds
4937	>10	U68385	Hs.117313	Human Meis1-related protein 2 (MRG2) mRNA partial cds
30795	>10	N53043	Hs.47606	ESTs
30966	>10	N59432	Hs.48382	EST-

**FIG.-7AV**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33991	>10	AA181935 M11591	Hs.104059	EST EST - M11591
2265	>10	W84413	Hs.23017	ESTs
24315	>10	AA608852	Hs.112603	EST
38752	>10	U79271	Hs.7571	Human clones 23920 and 23921 mRNA sequence
5119	>10	U44798	Hs.93502	Human U1-snRNP binding protein homolog mRNA complete cds
15037	>10	AA446000 AA459392 R44477 F03889	Hs.99043 Hs.105042 Hs.22646 Hs.27278	ESTs ESTs ESTs Highly similar to PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [Bos taurus Sus scrofa]
37045	>10	R92512	EST - RC_R92512_s	
37627	>10	N51987	Hs.47390	EST
21935	>10	AA001879	Hs.59890	EST
18669	>10	T52201	Hs.9410	ESTs
22737	>10	U90065	Hs.79351	Human two P-domain K+ channel TWIK-1 mRNA complete cds
30727	>10	AA148923	Hs.93675	ESTs
16086	>10	AA101056	EST - RC_AA101056	
23293	>10	AF001359	EST - AF001359_f	
5294	>10	U65093	Hs.82071	Human msig1-related gene 1 (mrg1) mRNA complete cds
17769	>10	AA214730	Hs.107256	ESTs
25549	>10	AA424535	Hs.98416	ESTs
84	>10	AA125781	Hs.57489	ESTs
4856	>10	AA442779	Hs.98983	ESTs
7697	>10	AA010619	Hs.16446	ESTs
36296	>10			
17490	>10			
36976	>10			
10425	>10			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41196	>10	R11654	Hs.20526	ESTs
42285	>10	T94409	EST - RC_T94409	
33185	>10	W69435	Hs.58009	EST
13974	>10	AA479299	Hs.21107	ESTs
19868	>10	H61560	EST - RC_H61560	
1378	>10	HG831-	EST - HG831-HT831	
621	>10	D63813	Human mRNA for rod photoreceptor protein complete cds	
5346	>10	U92459	Human metabotropic glutamate receptor 8 mRNA complete cds	
6029	>10	X66533	GUANYLATE CYCLASE SOLUBLE BETA-1 CHAIN	
22196	>10	R53972	HS.26026	ESTs
24609	>10	Z38900	HS.26615	ESTs
37196	>10	AA448226	EST - RC_AA448226	
26151	>10	AA250836	Hs.108509	ESTs
5938	>10	X62535	Diacylglycerol kinase alpha (80kD)	
16373	>10	AA019603	HS.74044	ESTs
28356	>10	AA609080	HS.60992	ESTs
20070	>10	H98854	HS.41585	ESTs
17717	>10	AA136541	HS.20423	ESTs
20069	>10	H98768	HS.71647	EST
40985	>10	N74604	HS.13121	ESTs
10194	>10	R63545	HS.124694	ESTs
			HS.11553	Weakly similar to putative type III alcohol dehydrogenase [D.melanogaster]
40200	>10	H87229	HS.82963	Gonadotropin-releasing hormone (leutinizing-releasing hormone)
34983	>10	AA347417	HS.96869	EST
23543	>10	T79203	HS.14480	ESTs
12770	>10	AA421778	HS.8861	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
25085	>10	AA017518	Hs.115241	Homo sapiens G protein beta 5 subunit mRNA complete cds
37746	>10	AA463627	Hs.99598	ESTs
2370	>10	M16505	Hs.79876	STERYL-SULFATASE PRECURSOR
31244	>10	N66062	Hs.49112	EST
31716	>10	N75507	Hs.50628	ESTs Weakly similar to CLATHRIN COAT ASSEMBLY PROTEIN
				AP17 [Rattus norvegicus]
28306	>10	AA598959	Hs.59163	ESTs
2220	>10	L76687	Hs.83070	Homo sapiens Grb14 mRNA complete cds
12404	>10	AA400292	Hs.23786	ESTs
41050	>10	N92882	Hs.109494	ESTs Weakly similar to putative progesterone binding protein [H.sapiens]
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR
23462	>10	T66948	Hs.12992	ESTs
18614	>10	F02418	Hs.107614	ESTs
40553	>10	N32060	Hs.104010	Homo sapiens CAG-isI 7 mRNA complete cds
27826	>10	AA455949	Hs.61232	ESTs
207	>10	D12763	Hs.66	Suppression of tumorigenicity 2
41064	>10	N93608	Hs.102923	EST
10845	>10	AA084405	Hs.106313	ESTs Weakly similar to P24 protein [M.musculus]
21813	10	R42039	Hs.23084	ESTs
18463	10	AA233151	Hs.81796	ESTs
17507	10	AA126419	Hs.74876	ESTs
23957	10	T97487	Hs.18070	ESTs
13317	10	AA448212	Hs.38095	ESTs
29550	10	H90133	Hs.41352	ESTs
39068	10	AA620411	Hs.141503	Small inducible cytokine A5 (RANTES)

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
26620	10	AA280413	Hs.89843	Spleen focus forming virus (SFV) proviral integration oncogene sp1
37675	10	AA460377	Hs.99816	ESTs
31437	10	N68821	Hs.49573	ESTs
32657	10	T66867	Hs.76889	ESTs
34952	10	AA342828	Hs.73734	PLATELET GLYCOPROTEIN V PRECURSOR
26475	10	AA262264	Hs.87640	ESTs
41827	10	T15445	Hs.99491	H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans
20073	10	H98985	Hs.111911	ESTs
42336	10	T99713	Hs.139933	ESTs
26412	10	AA258224	Hs.86646	ESTs
21352	10	R15880	Hs.21745	ESTs
22583	10	R79239	Hs.29855	EST
34020	10	AA191543	Hs.144302	EST
25913	10	AA161106	EST - RC_AA161106	
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
37531	10	AA456140	Hs.99235	ESTs
13314	10	AA448169	Hs.6728	ESTs
31430	10	N68610	EST - RC_N68610	
30570	10	N49587	Hs.46633	EST
7302	10	AA089688	Hs.103668	EST
27732	10	AA452167	Hs.55778	ESTs
22533	10	R73468	Hs.140996	ESTs
31079	10	N62969	Hs.48682	EST
35470	10	AA400393	Hs.97803	EST Weekly similar to precursor polypeptide [H.sapiens]
37102	10	AA446869	Hs.119316	ESTs

**FIG.-7Bc**

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
		ACCESSION	
203	10	D12620	CYTOCHROME P450 1Vf3
11427	10	AA233277	ESTs
24159	10	W57862	ESTs
17870	10	AA157772	ESTs
5302	10	U90543	Human butyrophilin (BTF1) mRNA complete cds
27256	10	AA417998	ESTs
2219	10	L76670	Homo sapiens nkaf7 mRNA complete cds
30858	10	N55081	EST
8870	10	AB002367	Human mRNA for KIAA0369 gene complete cds
40870	10	N67262	Zinc finger protein 135 (clone pHZ-17)
11811	10	AA258130	ESTs
33254	10	W72633	ESTs
17162	10	AA079094	EST - RC_AA079094
24392	10	W88568	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds
27456	10	AA430539	ESTs
25419	10	AA069386	EST - RC_AA069386
7100	10	AA012885	ESTs
31586	10	NT1571	ESTs
29995	10	N26401	EST
31973	10	N93875	EST
36159	10	AA419279	Colony-stimulating factor 1 (M-CSF)
12419	10	AA400888	ESTs
27076	10	AA401630	ESTs
28251	10	AA504512	ESTs Weakly similar to ZK792.1 [C.elegans]
4219	10	U32324	Human interleukin-11 receptor alpha chain mRNA complete cds

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27991	10	AA465650	Hs.87306	ESTs
37702	10	AA461119	Hs.99539	ESTs
25251	10	AA040792	Hs.54421	Bradykinin receptor B2
27064	10	AA401253	Hs.87677	ESTs
37592	10	AA458668	Hs.95898	ESTs
39619	9	F10640	Hs.12354	ESTs
31053	9	N62724	Hs.48614	EST
33338	9	W79524	Hs.58585	ESTs
23368	9	T59005	Hs.10476	EST
8240	9	AA397841	Hs.106879	ESTs
21778	9	R41389	Hs.26159	EST
31168	9	N63965	Hs.48903	ESTs
3440	9	S72370	Hs.89890	Pyruvate carboxylase
25930	9	AA164928	EST - RC_AA164928	
29971	9	N25657	Hs.93692	EST
39771	9	H17463	Hs.101735	ESTs
21481	9	R26141	Hs.24032	ESTs Highly similar to transmembrane receptor [M.musculus]
10887	9	AA101632	Hs.22971	ESTs
31431	9	N68666	Hs.76798	ESTs
30756	9	N52398	Hs.39252	ESTs
35829	9	AA411438	Hs.74635	Dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex 2-oxo-glutarate complex branched chain keto acid dehydrog
24540	9	Z30435	Hs.19235	ESTs
37500	9	AA455474	Hs.100530	ESTs
19007	9	H03358	EST - RC_H03358	

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42650	9	W92272	Hs.25601	Homo sapiens zinc-finger helicase (hZFH) mRNA complete cds
16705	9	AA043675	Hs.62633	EST
40275	9	H94647	Hs.102329	ESTs
24372	9	W87423	Hs.35598	ESTs
9011	9	CO1394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
40780	9	N59568	Hs.108107	ESTs
17177	9	AA079331		EST - RC_AA079331
20878	9	N70305	Hs.34492	ESTs
38140	9	AA486273	Hs.100472	ESTs
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
39112	9	AA620724	Hs.112890	ESTs
27347	9	AA424940	Hs.43590	ESTs
14747	9	D60364	Hs.34882	ESTs
23599	9	T82307		EST - RC_T82307
23979	9	T98262		EST - RC_T98262
27759	9	AA453472	Hs.95111	ESTs
36691	9	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIELE [H.sapiens]
26782	9	AA284181	Hs.89310	ESTs
26818	9	AA285145	Hs.50446	ESTs
22334	9	R61290	Hs.25870	ESTs
29892	9	N22995	Hs.42829	ESTs
22945	9	T10134	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
30618	9	N50656	Hs.93996	ESTs Highly similar to mosaic protein LR11 [H.sapiens]
29715	9	H98700	Hs.60887	ESTs
37560	9	AA457023		EST - RC_AA457023

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PRIMARY KEY	FOLD OF TUMOR vs.	DOWNREGULATED	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23264	9	T50062	Hs.9092	EST	
31001	9	N62200	Hs.47566	ESTs	
17841	9	AA156109	Hs.66180	ESTs	
3478	9	S76992	Hs.104005	Vav 2 oncogene	
11605	9	AA243139	Hs.4863	ESTs	
19032	9	H04822	Hs.30494	EST	
29933	9	N24182	Hs.93677	ESTs	
26622	9	AA280431	Hs.88756	ESTs	
4289	9	U35376	Hs.37138	Human repressor transcriptional factor (ZNF85) mRNA complete cds	
42034	9	T56281	Hs.110440	Human metallothionein (MT)-F gene	
30447	9	N47439	Hs.44603	ESTs	
25238	9	AA039568		EST - RC_AA039568	
20238	9	N30077	Hs.14855	ESTs	
30232	9	N34500	Hs.44600	EST	
17017	9	AA069920		EST - RC_AA069920	
11845	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]	
30229	9	N34457		EST - RC_N34457	
30737	9	N52137	Hs.47442	EST	
30555	9	N49259		EST - RC_N49259	
981	9	HG2139-		EST - HG2139-HT2208_f	
30498	9	N48325	Hs.93956	EST	
40434	9	N21461		EST - RC_N21461	
36788	9	AA435824	Hs.95594	Homo sapiens BAC clone RG113D17 from 7p14-p15	
28991	9	F04652	Hs.66195	ESTs	
25942	9	AA234187	Hs.87267	ESTs	

**FIG.-7Ba**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
30466	9	N47951	Hs.57485	ESTs
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]
13859	8	AA470066	Hs.24309	ESTs Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE MEDIUM CHAIN [Rattus norvegicus]
23445	8	T65992	Hs.11722	EST
24448	8	W93273	Hs.9270	ESTs Weakly similar to isopentenyl-diphosphate Delta-isomerase [H.sapiens]
7583	8	AA167824	Hs.63559	ESTs Highly similar to PROTEIN CDC27HS [Homo sapiens]
22778	8	R94840	Hs.35372	ESTs Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]
16439	8	AA024835	Hs.47584	Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA complete cds
42395	8	W42733	Hs.109870	ESTs
19991	8	H90887	Hs.18357	ESTs
23690	8	T87648		EST - RC_T87648
7111	8	AA018804	Hs.125175	ESTs Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]
6400	8	X86163	Hs.54421	Bradykinin receptor B2
42474	8	W63747	Hs.109918	H.sapiens: TTF mRNA for small G protein
11425	8	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds
27039	8	AA400277	Hs.48849	ESTs
32206	8	R44386	Hs.91703	ESTs
15310	8	W19098	Hs.7921	ESTs
36601	8	AA431337	Hs.98017	ESTs
463	8	D38462		EST - D38462
31674	8	N74357	Hs.50482	ESTs

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
31182	8	N64339	Hs.48956	EST
13499	8	AA453458	Hs.7301	ESTs
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1
5998	8	X65644	Hs.75063	HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2
962	8	HG180-N62328	Hs.3786	EST - HG180-HT180
40790	8	AA131512	Hs.103820	Glutamate receptor metabotropic 3
25700	8	AA436706	Hs.98895	ESTs
36880	8	M55267	Hs.41846	EVI2A PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2A PROTEIN)
2809	8	X14885	Hs.2025	Transforming growth factor beta 3
5620	8	AA039325	Hs.47200	ESTs
16643	8	R01450	Hs.91061	ESTs
32051	8	W90617	Hs.50120	ESTs
33550	8	X75535	Hs.118884	33 KD HOUSEKEEPING PROTEIN
6177	8	W45531	Hs.94642	ESTs
33000	8	H98701	Hs.4985	ESTs
20066	8	U50534	Hs.30649	Human infant brain mRNA clone 13cDNA73
4590	8	AA448257	Hs.97127	ESTs
37199	8	Z38844	Hs.25803	ESTs
24601	8	W93074	Hs.59342	ESTs
33589	8	AA453466	Hs.99330	ESTs
37389	8	X55448	Hs.3118	H.sapiens: mRNA for 2.19 gene
5801	8	D25912	Hs.74832	ESTs
28748	8	H72592	Hs.77554	ESTs
40070	8			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40367	8	H98857	Hs.75520	Human mRNA for KIAA0041 gene partial cds ESTs
33609	8	W93585	Hs.59476	ESTs
24502	8	Z38214	Hs.26946	ESTs
11129	8	AA156873	Hs.15970	ESTs
7144	8	AA033659	Hs.95154	ESTs
28584	8	C21221	Hs.68619	ESTs Highly similar to METALLOTHIONEIN-1A [Equus caballus]
22165	8	R52822	Hs.22003	ESTs
31987	8	N94551	Hs.55060	ESTs
32470	8	T15956	Hs.65289	EST
38642	8	AA5999152	Hs.91379	PTB-ASSOCIATED SPLICING FACTOR
40438	8	N21684	Hs.80500	Human mRNA for KIAA0061 gene partial cds
34471	8	AA258843	Hs.111376	ESTs
41571	8	R61005	Hs.115170	Homo sapiens mRNA for Gait4 protein
31417	8	N68435	Hs.49516	ESTs
23951	8	T97318	Hs.18037	ESTs
7832	8	AA249260	Hs.28545	ESTs
27928	8	AA461093	Hs.26799	Moderately similar to zinc finger protein [R.norvegicus]
2017	8	L34219	Hs.1933	Cellular retinaldehyde-binding protein
25530	8	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
20556	8	N55189	Hs.34081	ESTs
27096	8	AA400155	Hs.142935	ESTs
22651	7	R85266	Hs.33487	ESTs
33663	7	W95805	Hs.59736	EST
19374	7	H19472	Hs.31653	EST
10275	7	R79356	Hs.19280	ESTs Weakly similar to PROTEIN Q300 [Mus musculus]

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39471	7	D60265 AA019426	Hs.107894 Hs.103343	ESTs EST
25100	7	AB002316 AA075674	Hs.65746	Human mRNA for KIAA0318 gene partial cds EST - RC_AA075674
8828	7	Y09858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical protein
17132	7			
15915	7			
8216	7	AA393089 R71489	Hs.86723 Hs.29196	ESTs EST
22512	7	H08171	Hs.30842	ESTs
19097	7	AA011041	Hs.130843	ESTs
25048	7	AA398962	Hs.97699	ESTs
35353	7	N66399	Hs.49193	EST
31278	7	T26893	Hs.7569	EST
23149	7	AA262783	Hs.22057	ESTs
11880	7	AA127595	Hs.71016	ESTs
17547	7	W32094	Hs.55501	ESTs
32854	7	AA435978	Hs.98852	EST
36822	7	AA400893	Hs.41717	Human 3' cyclic nucleotide phosphodiesterase (HSPDE A3A) mRNA complete cds
35530	7	U14417	Hs.106185	Human F1 guanine nucleotide dissociation stimulator mRNA partial cds
3869	7	H09246 U79527	Hs.100739 Hs.111075	ESTs Human orphan G-protein coupled receptor Dez isoform a mRNA complete cds
9368	7			
15154	7			
21178	7	R06607	Hs.19748	EST-

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33081	7	W57731	Hs.56213	ESTs
13848	7	AA465664	Hs.21323	ESTs
18659	7	FO3220	Hs.13258	ESTs
1979	7	L29339	Hs.1964	Solute carrier family 5 (sodium/glucose cotransporter) member 1
22609	7	R80945	Hs.29978	ESTs
2418	7	M19507	Hs.1817	Myeloperoxidase
28863	7	D80051	Hs.124418	ESTs
26764	7	AA283926	Hs.51501	ESTs
6544	7	X95677	EST - XE5677	
33524	7	W89188	Hs.59096	ESTs
18374	7	AA226877	Hs.67624	ESTs
10108	7	R25069	Hs.23790	ESTs
26178	7	AA251153	Hs.27910	Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA complete cds
36428	7	AA427605	Hs.98551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds
29808	7	N21032	Hs.42931	EST
24837	7	Z41186	Hs.27997	ESTs
24909	7	Z98492	Hs.27250	ESTs
26333	7	AA256075	Hs.82280	Homo sapiens regulator of G protein signalling 10 mRNA complete cds
11507	7	AA235465	Hs.29161	ESTs
40387	7	H99460	Hs.108873	ESTs
16112	7	AA004377	Hs.91813	Human b-tyrophilin (BTF2) mRNA complete cds
25413	7	AA065096	EST - RC_AA065096	

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
13232	7	AA443844	Hs.20887	ESTs
27236	7	AA417037	Hs.67805	ESTs
21684	7	R38944	Hs.129672	ESTs Weakly similar to ANK repeat region of
9294	7	D82712	Hs.15301	Fowlpox virus BamHI-orf7 protein [C.elegans]
16886	7	AA057119	Hs.5091	Homo sajiens torsinB (DQ1) mRNA partial cds
20083	7	H99879	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]
30651	7	N51029	Hs.38672	ESTs
22362	7	R62447	Hs.22123	ESTs
21561	7	R33245	Hs.23076	ESTs
21636	7	R37501	Hs.23600	ESTs
21223	7	R08175	Hs.110130	Homo sajiens chromosome 19 cosmid F22329
32218	7	R45654	Hs.1339	Collagen type IV alpha 2
13405	7	AA450118	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]
30627	7	N50740	Hs.47111	ESTs
30117	7	N30824	Hs.44227	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
31344	7	N67238	EST - RC_N67238	
38119	7	AA485714	Hs.105669	ESTs
33297	7	W73781	Hs.105715	ESTs
6892	7	Z30426	Hs.82401	CD69 antigen (early T cell activation antigen)
9923	7	N44998	Hs.24550	ESTs
27942	7	AA463237	Hs.13021	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34845	7	AA293420	Hs.95464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]
29829	7	N21460	Hs.43005	ESTs
15059	7	U53831	Hs.85280	Human interferon regulatory factor 7 (humirf7) mRNA complete cds
40441	7	N22053	Hs.112083	ESTs
25095	7	AA018937	Hs.109558	ESTs
2941	7	M62840	Hs.82542	Acyloxyacyl hydrolase (neutrophil)
1945	7	L25878	Hs.89649	Epoxide hydrolase 1 microsomal (xenobiotic)
42648	7	W92150	Hs.79310	Human G1AP SH3 binding protein mRNA complete cds
19592	7	H40696	Hs.33790	ESTs
29801	7	N20939	Hs.38759	ESTs
15417	7	W26982	Hs.39330	ESTs
39877	7	H38627	Hs.107696	ESTs
23967	7	T97910	Hs.18184	EST
20041	7	H97012	Hs.11050	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]
18314	7	AA214510	Hs.86618	ESTs
22452	7	R67370	Hs.28758	ESTs
30496	7	N48294	Hs.46850	EST
26830	7	AA287057	Hs.48820	ESTs
33432	7	W86075	Hs.38715	ESTs
31394	7	N67990	Hs.49421	ESTs
7053	6	Z84721	Hs.75792	Hemoglobin alpha 1
33518	6	W88996	Hs.59134	EST
5355	6	U94320	Hs.123021	Human Y5 receptor mRNA complete cds
41311	6	R38516	Hs.124255	EST

**FIG.-7Bn**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
12545	6	AA406320	Hs.24702	ESTs
23843	6	T92561	Hs.110422	ESTs
21667	6	R38475	Hs.21408	ESTs
17472	6	AA121704	Hs.69494	ESTs
25648	6	AA126673	Hs.110341	ESTs
32710	6	T87324	Hs.91021	EST
3450	6	S73840	Hs.931	H.sapiens mRNA for fast 2a myosin heavy chain (3' end)
979	6	HG2090-		EST - HG2090-HT2152
8151	6	AA348686		EST - AA348686
35380	6	AA399522	Hs.97671	ESTs Weakly similar to T04A8.9 [C.elegans]
23798	6	T91047	Hs.126785	ESTs
940	6	HG1496-		EST - HG 1496-HT1496
35896	6	AA412106	Hs.97349	ESTs
16350	6	AA019034	Hs.94000	ESTs
27547	6	AA436613	Hs.72157	ESTs
22528	6	R73036	Hs.29323	EST
25815	6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]
8473	6	AA437346	Hs.2967	SHB adaptor protein (a Src homology 2 protein)
35742	6	AA406058	Hs.97999	EST
36538	6	AA430002	Hs.112044	ESTs
17831	6	AA152323	Hs.71947	ESTs
25072	6	AA015799	Hs.33792	ESTs
15632	6	W56102	Hs.71218	ESTs
20442	6	N50827	Hs.25275	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28357	6	AA609120	Hs.56185	ESTs Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase. [H.sapiens]
25022	6	AA007591 H68158	Hs.110227 Hs.28310	ESTs ESTs
29334	6	AA488875	Hs.6433	Homo sajiens clone 24523 mRNA sequence
28148	6	N52195	Hs.105365	H.sapiens mRNA for arginine methyltransferase
30744	6	AA442090	Hs.119295	ESTs
27577	6	W87469	Hs.58992	ESTs
33472	6	AA130867	Hs.100119	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING
25687	6	AA027317	Hs.19136	ENTRY !!! [H.sapiens]
10549	6			ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING
32836	6	W23631	Hs.55426	ESTs
17025	6	AA070160	Hs.4217	EST - RC_AA070160
22939	6	T10070	X52332	Homo sapiens mRNA for KIAA0667 protein partial cds
15803	6		Hs.104115	Human Kox1 gene for zinc finger protein
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA.
11074	6	AA148983	Hs.29068	ESTs
12212	6	AA297746	Hs.22654	ESTs
16102	6	AA002150	Hs.59872	ESTs
31340	6	N67197	Hs.50125	EST
19459	6	H24317	Hs.6526	ESTs
17533	6	AA127098	Hs.71057	EST
22017	6	R46597	Hs.22703	ESTs
23687	6	T87519	Hs.16075	ESTs Weakly similar to no similarities to reported gene products [H.sapiens]
30298	6	N36130	Hs.44792	EST Weakly similar to hypothetical protein [H.sapiens]

**FIG.-7B**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28973	6	F04014	Hs.65996	ESTs
17042	6	AA070397		EST - RC_AA070397
20817	6	N68628	Hs.37630	ESTs
18430	6	AA232138	Hs.118898	ESTs
28493	6	C14820	Hs.67186	EST
30497	6	N48302	Hs.46852	EST
32502	6	T16896	Hs.65373	ESTs
41324	6	R38804	Hs.13434	Homo sapiens clone 24418 mRNA sequence
18418	6	AA228096	Hs.60480	ESTs
23622	6	T84046	Hs.15345	ESTs
15342	6	W25781	Hs.8136	Homo sapiens clone 23698 mRNA sequence
15246	6	W01094	Hs.84628	ESTs
2247	6	M10321	Hs.110802	VON WILLEBRAND FACTOR PRECURSOR
31906	6	N92643	Hs.35986	Homo sapiens CASK mRNA complete cds
9062	6	C06238	Hs.95665	Homo sapiens clone 24700 unknown mRNA partial cds
38640	6	AA599142	Hs.112509	EST
42622	6	W87801	Hs.108209	ESTs
27908	6	AA460671	Hs.54837	EST - AA085354
7293	6	AA085354		
27322	6	AA424325	Hs.40496	Phosphoribosylglycinamide formyltransferase
5774	6	X54199	Hs.822285	phosphoribosylaminoimidazole synthetase
33469	6	W87454	Hs.58987	ESTs Highly similar to homogentisate 12-dioxygenase [H.sapiens]
40329	6	H97488	Hs.108802	Human N-ethylmaleimide-sensitivity factor mRNA partial cds
26539	6	AA278848	Hs.88522	ESTs

**FIG\_7Ba**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23579	6	T81098 R66706	Hs.124065 Hs.28706	ESTs ESTs
22435	6	H80842	Hs.37445	ESTs
19956	6	F02345	Hs.21197	ESTs
18607	6	H02554	Hs.30323	ESTs
18991	6	AA248169	Hs.106709	ESTs Highly similar to LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR [Rattus norvegicus]
7810	6	N53419 AA169606 AA252357 AA449267	Hs.47646 Hs.72815 Hs.87794 Hs.17914	ESTs ESTs ESTs EPSILON RECEPTOR BETA-SUBUNIT [M.musculus]
30810	6	U43701	Hs.75403	60S RIBOSOMAL PROTEIN L23A
17996	6	Z41058	Hs.79248	ESTs
26245	6	W84432	Hs.58670	ESTs
13348	6	N64017	Hs.48911	ESTs
15034	6	N64144	Hs.102749	EST
33802	6	L13258	Hs.936	Solute carrier family 17 (sodium phosphate) member 2
33394	6	AA142922	Hs.9817	Homo sapiens Arg/Abl-interacting protein ArgBP2a (ArgBP2a)
31170	6			mRNA complete cds
40828	6			
1789	6			
17740	5			
9509	5	H58970	Hs.49683	ESTs
15540	5	W30895	Hs.7535	ESTs
27827	5	AA455976	Hs.42355	ESTs
30697	5	N51585	Hs.47049	ESTs
40299	5	H95787	Hs.108745	ESTs

FIG.-7Br

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
16627	5	AA036779 N62915	Hs.61826 Hs.57672	Homo sapiens clone 23928 mRNA sequence ESTs Weakly similar to weakly similar to myosin heavy chain [C.elegans]
20659	5	N62272 T65508 N63178 R98421	Hs.48502 Hs.14623 Hs.48728	ESTs Homo sapiens mRNA for KIAA0625 protein partial cds ESTs ESTs
31009	5	AA040507	Hs.92924	ESTs - RC_R98421
14877	5	R38910 AA464626 AA262974	Hs.66170 Hs.10247 Hs.111394	ESTs Homo sapiens clone 24503 mRNA sequence Activated leucocyte cell adhesion molecule ESTs
31102	5	H88338 R40974 AA400514	Hs.90250 Hs.124270 Hs.97505	ESTs ESTs ESTs
22830	5	AA459649 AA404282	Hs.99485 Hs.63481	ESTs Weakly similar to kynureine/alpha-amino adipate aminotransferase [R.nonvegicus] EST - RC_AA082933
25248	5	AA082933 D50930 AA122394	Hs.5084 Hs.70811	Human mRNA for KIAA0140 gene complete cds ESTs
32145	5	X80878 U77845 T23513	Hs.95262 Hs.21254 Hs.7147	Human R kappa B mRNA complete cds Human hTRIP (hTRIP) mRNA complete cds ESTs
27970	5	D80990 R76401 W70259	Hs.45247 Hs.92262 Hs.48523	ESTs ESTs ESTs
34509	5			
29522	5			
32159	5			
35492	5			
37630	5			
27103	5			
17209	5			
589	5			
17489	5			
6293	5			
5067	5			
23060	5			
28902	5			
32328	5			
33218	5			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
28751	5	D45455 R19360	Hs.65524 Hs.14651	ESTs
21400	5	W36290	Hs.9115	ESTs
15557	5	AA412293	Hs.21258	ESTs
12631	5	R62579	Hs.62264	ESTs
32282	5	AA009809	Hs.37599	ESTs
10416	5	H96306	Hs.32980	Human mRNA for BST-1 complete cds
40308	5	AA242829	Hs.7508	ESTs
11599	5	W70279	Hs.94811	ESTs Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]
33220	5	T23867 W24154	Hs.7316 Hs.6166	ESTs
23100	5	AA412556	EST - AA412556	
15333	5	C01360	Hs.67364	Homo sapiens clone 23904 mRNA sequence
8331	5	U53225	Hs.75283	Sorting nexin 1
9010	5	AA035444	Hs.100543	Homo sapiens clone 24505 mRNA sequence
4660	5	AA039933	Hs.30941	Myasthenic syndrome antigen B [human fetal brain mRNA 3477 nt]
25213	5	D20538	Hs.90165	EST
25242	5	AA096412 D14823	Hs.26236 Hs.101442	ESTs
28708	5	A099580	Hs.101442	ESTs Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]
7435	5	X04571	Hs.2230	EST - D14823
25538	5	F10040	Hs.13251	Epidermal growth factor
271	5	T62918	Hs.11110	ESTs
5490	5	T66282	Hs.12907	ESTs Weakly similar to ZINC FINGER PROTEIN 42 [H.sapiens]
18812	5			
23393	5			
23446	5			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
35204	5	AA3998155	Hs.97600	ESTs
31369	5	N67598	Hs.136395	ESTs
5244	5	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds
20835	5	N69215	Hs.37456	ESTs
16502	5	AA027059	Hs.61425	EST
23691	5	T87693	Hs.16414	ESTs
31842	5	N90168	Hs.54593	EST
7845	5	AA249611	EST - AA:249611	
29297	5	H65459	Hs.38323	ESTs
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIAA0554 protein partial cds
36412	5	AA426464	Hs.98466	ESTs
19357	5	H18929	EST - RC_H18929	
16299	5	AA016258	EST - RC_AA016258	
25312	5	AA047078	Hs.95278	ESTs Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!!-[H.sapiens]
27617	5	AA446114	Hs.55409	ESTs
42432	5	W46403	Hs.107293	ESTs
38432	5	AA496983	Hs.78672	Laminin alpha 4
32215	5	R45175	Hs.117183	ESTs
15214	5	U93553	Hs.91310	Human alpha1-fetoprotein transcription factor (hFTF) mRNA complete cds
15141	5	U78798	Hs.90957	Human TNF receptor associated factor 6 (TRAF6) mRNA complete cds
20052	5	H97922	Hs.5376	Human LXR-interacting protein 1a mRNA complete cds
7551	5	AA156838	Hs.107941	ESTs
26451	5	AA259058	Hs.43616	ESTs

**FIG.-7Bu**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42355	5	W20404	Hs.55405	ESTs
39480	5	D60419	Hs.81915	STATMIN
17369	5	AA101833	Hs.69293	EST
14993	5	U22172	Hs.73046	Human DNA damage repair and recombination protein RAD52 pseudogène mRNA partial cds
23400	5	T63336	Hs.105095	ESTs
21153	5	R05315		EST - RC_R05315
14282	5	AA505141	Hs.11923	ESTs
21104	5	R01081		EST - RC_R01081
32825	5	W20364	Hs.55412	ESTs
35018	5	AA349591		EST - RC_AA349591
25104	5	AA019598	Hs.103351	ESTs
19235	5	H12725	Hs.31181	ESTs
34979	5	AA347209	Hs.7841	Human miRNA for KIAA0324 gene partial cds
21501	5	R26855	Hs.24120	ESTs
18331	5	AA218543	Hs.10881	Homo sapiens mRNA for KIAA0541 protein partial cds
37529	5	AA456112	Hs.99410	ESTs
15532	5	W28944	Hs.5296	ESTs Highly similar to PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN BISC-CSPA INTERGENIC REGION [Escherichia coli]
11858	5	AA262308	Hs.106385	ESTs
29450	5	H80865	Hs.111026	Phosphatidylinositol glycan class F
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY
35170	5	AA397830	Hs.98347	RESPONSE PROTEIN MYD118 [Mus musculus]
23201	5	T40652	Hs.8279	ESTs Weakly similar to rtp-1 [H.sapiens]

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27012	5	AA398913	Hs.45231	ESTs
28767	5	D45608	Hs.83792	Surfactant pulmonary-associated protein D
17777	5	AA149634	Hs.62788	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
20588	5	N58009	Hs.36218	ESTs
20356	5	N39453	Hs.27371	ESTs
23375	5	T59670	Hs.10615	EST
17030	5	AA070188		EST - RC_AA070188
30752	5	N52340	Hs.118084	EST
25808	5	AA149226	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
31345	5	N67268	Hs.50139	ESTs
30784	5	N52857	Hs.47558	ESTs
13707	5	AA460281	Hs.14697	ESTs
29199	5	H25761	Hs.57082	EST
39003	4	AA609920	Hs.112785	EST
41529	4	R54458	Hs.2699	Glypican 1-
3151	4	M83652	Hs.53155	Properdin P factor complement
33134	4	W61264	Hs.57829	ESTs
29196	4	H24456	Hs.85053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27973	ESTs
11949	4	AA279827	Hs.125035	ESTs
31925	4	N92924	Hs.125032	ESTs
35258	4	AA398428	Hs.97628	ESTs
39838	4	H27216	Hs.107635	ESTs
30796	4	N53046	Hs.91146	Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
19464	4	H24458	Hs.32085	EST

FIG.-7BW

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
42486	4	W68410 AA236352	Hs.106857 Hs.110821	Calbindin 2 (29kD calretinin) ESTs
34274	4	AA459917	Hs.99506	EST
37648	4	M85085	Hs.693	Cleavage stimulation factor 3' pre-RNA subunit 2 64kD ESTs
3169	4	R96417	Hs.107795	ESTs
10326	4	U56814	Hs.88646	Homo sapiens DNase gamma mRNA complete cds ESTs
15063	4	T80628	Hs.108169	ESTs
23571	4	AA599583	Hs.15299	ESTs Weakly similar to HSM-2 [H.sapiens]
14377	4	R56239	Hs.6666	ESTs
22255	4	AA435968	Hs.98849	ESTs Weakly similar to bithoraxoid [D.melanogaster] EST
36820	4	AA358015	Hs.96998	ESTs
35063	4	AA399271	Hs.19610	ESTs
12376	4	N68163	Hs.49455	ESTs
31406	4	AA429028	Hs.42676	ESTs Moderately similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!! [H.sapiens]
27430	4	N40170	Hs.45046	ESTs
30362	4	N50039	Hs.47004	ESTs
30599	4	AA460319	Hs.48469	ESTs
27894	4	N90218	Hs.54607	ESTs
31844	4	AFFX-	AFFX-HUMGAPDH/M33197_M	
24935	4	N68829	Hs.131510	ESTs
40906	4	AA398246	Hs.97594	ESTs
35220	4	N94832	Hs.121699	ESTs
10024	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds EST
4238	4	AA256396	Hs.88156	EST
26358	4	Z39734	Hs.22550	ESTs
24716	4			

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19243	4	H13539	Hs.31222	ESTs
41844	4	T15833	Hs.100227	EST
39774	4	H17948	Hs.106311	Homo sapiens DGS-A mRNA 3' end
20111	4	N21380	Hs.25497	H.sapiens mRNA for ROX protein
24008	4	T99337	Hs.18624	ESTs
8316	4	AA410529	Hs.30732	ESTs
35072	4	AA358738		EST - RC_AA358738
39794	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence
1517	4	J04501	HS.772	Glycogen synthase 1 (muscle)
9164	4	D38081	HS.89887	Thromboxane A2 receptor
35027	4	AA349996	HS.96937	ESTs
35185	4	AA398015	HS.97590	Untitled
26570	4	AA279425	HS.86428	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
19759	4	H54352	HS.36873	ESTs
34310	4	AA243416	HS.75470	Homo sapiens mRNA expressed in osteoblast complete cds
39961	4	H57317	HS.108161	ESTs
23249	4	T47919	HS.8749	ESTs
19119	4	H09077	HS.30895	EST
14158	4	AA490182	HS.118598	ESTs
22866	4	R99938	HS.36189	EST
16935	4	AA059392	HS.66779	ESTs
41950	4	T33137	HS.7967	ESTs
20404	4	N48694	HS.30881	Homo sapiens liprin-alpha2 mRNA complete cds
18406	4	AA227962	HS.112075	ESTs Weakly similar to reverse transcriptase [M.musculus]
16560	4	AA031308	HS.24341	ESTs
26098	4	AA242831	HS.87606	ESTs

FIG.-7Bv

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
34360	4	AA251547	Hs.104358	EST
16830	4	AA054222	Hs.40400	ESTs
32668	4	T69284	Hs.2314	Mannose-binding lectin soluble (opsonic defect)
32912	4	W38051	EST - RC_W38051	
16230	4	AA011549	Hs.47884	ESTs
29696	4	H97909	Hs.42344	ESTs
8232	4	AA397529	EST - AA397529	
25584	4	AA112320	Hs.16704	ESTs
30878	4	N56882	Hs.46761	EST
40579	4	N34524	Hs.102516	ESTs
8026	4	AA301842	Hs.105189	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]
3094	4	M77481	Hs.72879	Human antigen (MAGE-1) gene complete cds
17480	4	AA121974	EST - RC_AA121974	
15766	4	W95777	Hs.90804	ESTs
34865	4	AA299903	Hs.111498	EST
29779	4	N20290	Hs.42836	ESTs
6547	4	X95808	Hs.9568	Human mRNA for KIAA0385 gene complete cds
24479	4	W96222	Hs.34192	ESTs
16135	4	AA004805	Hs.63668	Human Toll-like receptor 2 (TLR2) mRNA complete cds
11098	4	AA151243	Hs.38163	ESTs
14388	4	AA599742	Hs.21600	ESTs
36078	4	AA417275	Hs.98214	ESTs
23440	4	T65566	Hs.12859	ESTs
20863	4	N69989	Hs.19167	ESTs
20347	4	N39117	Hs.12250	ESTs
7795	4	AA247455	Hs.15220	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10729	4	AA054087	Hs.18858	ESTs
12734	4	AA419200	Hs.5737	ESTs
24446	4	W93119	Hs.19512	ESTs
30734	4	N52083	Hs.47418	EST
20641	4	N62353	Hs.109685	ESTs
21183	4	R06769	Hs.19795	ESTs
18138	4	AA192757	Hs.131687	ESTs
35310	4	AA398662	Hs.97302	ESTs
39497	4	D80154	Hs.56340	ESTs
29866	4	N22343	Hs.43145	ESTs
8707	4	AA479995	Hs.76982	Homo sapiens mRNA for KIAA0583 protein partial cds
18472	4	AA233299	Hs.72158	ESTs
24720	4	Z39754	Hs.23236	ESTs
40825	4	N63923	Hs.102746	ESTs
15375	4	W26395	Hs.56876	ESTs
32869	4	W35211	Hs.54801	ESTs
4641	4	U52426	Hs.74597	Homo sapiens GOK (STIM1) mRNA complete cds
11786	4	AA256616	Hs.31707	ESTs
21571	4	R33841	Hs.24709	Homo sapiens GOK (STIM1) mRNA complete cds
1600	4	K03474	EST - K03474	EST - K03474
21103	4	R01068	Hs.14603	ESTs
22993	4	T16358	Hs.106443	ESTs
38666	4	AA599661	Hs.103849	ESTs
27148	4	AA406231	Hs.100113	Human mRNA for KIAA0381 gene partial cds
28680	4	D20261	Hs.80067	ESTs
36397	4	AA426372	Hs.109804	Human mRNA for histone H1x complete cds

**FIG.-7Ca**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
26915	4	AA330634		EST - RC_AA330634
6912	4	Z35278	Hs.2536	H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA
31825	4	N89848	Hs.54543	ESTs
10763	4	AA057620	Hs.30807	ESTs
17007	4	AA069696	Hs.67317	ESTs
33439	4	W86445	Hs.58844	ESTs
27657	4	AA447612	Hs.60435	ESTs
26288	4	AA253393	Hs.87734	ESTs
8235	4	AA397616	Hs.107245	ESTs Moderately similar to potassium channel protein Raw3 [R.norvegicus]
12114	4	AA287097	Hs.25114	ESTs
879	4	D88155	Hs.97196	Human steroidogenic factor 1 mRNA complete cds
30793	4	N52979	Hs.51919	Plasminogen-like protein
13522	4	AA454115	Hs.6000	ESTs
20819	4	N68730	Hs.12160	ESTs
20019	4	H94266	Hs.9451	ESTs
32396	4	R95778	Hs.93008	EST
38162	4	AA487165	Hs.105706	EST
8487	4	AA442669	EST - AA442669	
18444	4	AA232646	Hs.68061	ESTs
16183	4	AA010070	Hs.60339	EST
33047	4	W49755	Hs.89359	ESTs Moderately similar to type Ia hair keratin a3 [H.sapiens]
14797	4	S82769	Hs.104133	GABAA receptor gamma 3 subunit [human fetal brain mRNA Partial 1536 nt]
26107	3	AA243172	Hs.87619	ESTs
24421	3	W92001	Hs.120969	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
27665	3	AA447759	Hs.134724	ESTs
19154	3	H10047	Hs.22515	ESTs
10933	3	AA121360	Hs.27567	ESTs Weakly similar to alpha-13-mannosyl-glycoprotein beta-1 2-N-acetylglucosaminyltransferase [C.elegans]
7254	3	AA074897		EST - AA074897
18684	3	F04262	Hs.22137	ESTs
40997	3	N77904	Hs.44380	ESTs
14971	3	U10493	Hs.438	Human Mox1 protein (MOX1) mRNA complete cds
11217	3	AA180487	Hs.62440	ESTs
16782	3	AA047265	Hs.82582	Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds
21477	3	R26094	Hs.23531	ESTs
21382	3	R16896	Hs.89615	PROTEIN KINASE C THETA TYPE
19508	3	H28966		EST - RC_H28966
30301	3	N36174	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR
21553	3	R33005	Hs.23153	ESTs Weakly similar to ETX1 {alternatively spliced} [H.sapiens]
6102	3	X70340	Hs.2023	Transforming growth factor alpha
23502	3	T70580	Hs.13759	ESTs
8333	3	AA412620	Hs.4248	ESTs
30500	3	N48329	Hs.30490	F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]
21431	3	R22057	Hs.23336	ESTs
35920	3	AA412290	Hs.98124	ESTs
12065	3	AA283907	Hs.110480	Homo sapiens clone 23837 mRNA sequence
19156	3	H10068	Hs.25924	Homo sapiens clone 24466 mRNA sequence
24844	3	Z41301	Hs.23539	ESTs

**FIG.-7Cc**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
33178	3	W68846	Hs.141719	
2052	3	L36818	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)
15327	3	W23474	Hs.23352	ESTs
18874	3	F10565	Hs.12345	ESTs
9039	3	C02049	Hs.106291	ESTs
37470	3	AA454935	Hs.99566	ESTs
19167	3	H10641	Hs.22928	ESTs
34888	3	AA303078	Hs.94479	Human Gt334 protein (GT334) gene mRNA complete cds
30591	3	N49952	Hs.138717	ESTs
26997	3	AA398488	Hs.93090	ESTs
18647	3	F03004	Hs.27109	ESTs
17867	3	AA157291	Hs.72163	ESTs
15280	3	W07019	Hs.35088	ESTs
20465	3	N51599	Hs.14633	ESTs
11047	3	AA142849	Hs.22660	ESTs
19451	3	H23747	Hs.31697	ESTs
41621	3	R69233	Hs.101504	ESTs
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I
28675	3	D20188	Hs.74876	ESTs
13928	3	AA478441	Hs.11590	ESTs
29473	3	H83694	Hs.40478	ESTs
25829	3	AA151621	Hs.110964	ESTs
28532	3	C20680	Hs.68513	EST
32376	3	R91391	Hs.64391	ESTs
12064	3	AA283848	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]
15547	3	W32012	Hs.29353	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
40284	3	H95073	Hs.108734	ESTs Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]
22861	3	R99595	Hs.36152	ESTs
15525	3	W28763	Hs.16349	Homo sapiens KIAA0431 mRNA partial cds
17968	3	AA167496	Hs.72695	EST
3836	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
4528	3	U48251	Hs.75871	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds
29784	3	N20468	Hs.42849	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]
7892	3	AA262100		EST - AA262100
15279	3	W05746	Hs.133302	ESTs
42064	3	T63364	Hs.9225	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parvimensis]
17943	3	AA165117	Hs.20509	ESTs
4596	3	U50743	Hs.19520	Sodium/potassium ATPase gamma subunit
16421	3	AA022541	Hs.61146	ESTs
4914	3	U67611		EST - U67611
38171	3	AA487301	Hs.105713	EST
20168	3	N24106	Hs.2799	Cartilage linking protein 1
18791	3	F09892	Hs.12575	ESTs
24281	3	W79773	Hs.16511	ESTs
13996	3	AA480907	Hs.15769	ESTs
20583	3	N57797	Hs.34421	ESTs
37181	3	AA448158	Hs.99152	EST
21450	3	R23146	Hs.23466	ESTs
19634	3	H44866	Hs.31597	ESTs

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10163	3	R54534	Hs.7898	Homo sapiens clone 23938 mRNA sequence
7059	3	Z96810	Hs.911797	EST - Z96810
25762	3	AA136066	Hs.92897	Retinoblastoma-binding protein 1 {alternative products}
27426	3	AA428900	Hs.92897	ESTs
29023	3	F09302		EST - RC_F09302
10989	3	AA132366	Hs.8023	Homo sapiens mRNA for SP0P
6587	3	X97748		EST - X97748
8722	3	AA481309	Hs.30204	ESTs
21476	3	R26065	Hs.23523	ESTs
14096	3	AA487558	Hs.8135	ESTs
35392	3	AA399562	Hs.97566	ESTs
28608	3	C21509	Hs.112774	ESTs
13350	3	AA449297	Hs.8944	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]
41202	3	R12808	Hs.113619	ESTs
15612	3	W51955	Hs.73372	ESTs
33930	3	AA169539	Hs.95870	ESTs
34215	3	AA233855	Hs.104252	UTROPHIN
19208	3	H11734	Hs.110454	ESTs Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]
24047	3	W15386	Hs.26750	ESTs
14852	3	T52099	Hs.100383	ESTs Highly similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [Rattus norvegicus]
27815	3	AA455370	Hs.59729	ESTs
22610	3	R81173	Hs.11482	ESTs Highly similar to F11 antigen [H.sapiens]
37510	3	AA455896	Hs.2699	Glypican 1

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
37825	3	AA470073 AA448238	Hs.104836 Hs.16714	ESTs ESTs
13321	3	AA235375	Hs.87421	EST
25999	3	M13150	Hs.99900	MAS1 oncogene
9738	3	AA013125	Hs.40871	ESTs
16248	3	AA442856	Hs.61979	ESTs Moderately similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [H.sapiens]
27582	3			ESTs
16546	3	AA029452 AA064859	Hs.95162 Hs.23161	EST - RC_AA064859 Homo sapiens retinoic acid hydroxylase mRNA complete cds
16981	3	R51021		EST - RC_T54617
22128	3	T54617		ESTs
23312	3	F09741	Hs.124205	ESTs
18783	3	R86920	Hs.127585	ESTs
10308	3	R71892	Hs.25996	ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]
22518	3			ESTs Weakly similar to estrogen-responsive finger protein efp [H.sapiens]
8255	3	AA400226	Hs.25024	ESTs Moderately similar to proto-cadherin 3 [R.norvegicus]
16361	3	AA019218	Hs.40550	Tumor necrosis factor
5453	3	X02910	Hs.2037	
22509	3	R71393	Hs.29190	ESTs
20065	3	H98657	Hs.27291	ESTs
31091	3	N63076	Hs.138746	EST
39050	3	AA610112	Hs.124849	ESTs
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM
30159	3	N32623	Hs.44069	ESTs
28913	3	F01560	Hs.22583	ESTs Highly similar to co-repressor protein [M.musculus]

FIG.-7Ca

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs. 	UNIGENE CLUSTER	UNIGENE CLUSTER	UNIGENE DESCRIPTOR	
				ACCESSION	UNIGENE CLUSTER
12257 359	3	AA350030 D26350	Hs.4221 Hs.75119	ESTs	Human rRNA for type 2 inositol 145-trisphosphate receptor complete cds
23587	3	T81358	Hs.14906	ESTs	
14323	3	AA598575	Hs.12851	ESTs	
27231	3	AA416936	Hs.7491	mRNA complete cds	Homo sapiens methionine synthase reductase [MTRR]
34914	3	AA338729 R08359	Hs.133096 Hs.19308	ESTs	
21233	3	T86475	Hs.16193	ESTs	
23660	3	AA496891	Hs.5011	ESTs	
14236					
17617	3	AA131394	Hs.44672	ESTs	Weakly similar to The KIAA0147 gene product is related to S.pombe rad21 gene product. [H.sapiens]
24594	3	Z38804	Hs.22555	ESTs	Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase. [H.sapiens]
7426	3	AA095885	Hs.111818	ESTs	Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
34871 17962	3	AA300151 AA167051	Hs.125146 Hs.83525	ESTs	Homo sapiens heat shock factor binding protein 1 HSPB1 mRNA complete cds
24337	3	W86007	Hs.8876	ESTs	
22589	3	R79580	Hs.29874	ESTs	
24554	3	Z38522	Hs.27082	EST	
22348	3	R61750	Hs.6136	ESTs	
30217	3	N34288	Hs.44554	EST	

FIG.\_7Ch

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
10210	3	R67468	Hs.131828	ESTs
22156	3	R52145	Hs.25894	ESTs
16404	3	AA021284	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]
29310	3	H66642	Hs.88729	ESTs
15956	3	Z21217	Hs.77695	Human mRNA for KIAA0008 gene complete cds
9758	3	M26393	Hs.127610	Acy-Coenzyme A dehydrogenase C-2 to C-3 short chain
20917	3	N72295	Hs.18004	ESTs
4847	3	U64573	EST - U64573	
22964	3	T10362	Hs.57958	ESTs
9806	2	M79462	Hs.89633	Probable transcription factor PML {alternative products}
29807	2	N21031	Hs.42930	ESTs
39646	2	H02255	Hs.7268	Homo sapiens clone 23872 mRNA sequence
22733	2	R92181	Hs.34558	EST
23233	2	T41177	Hs.8410	Homo sapiens retinoic acid-inducible endogenous retroviral DNA
18549	2	F01360	Hs.6092	ESTs Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]
31892	2	N91968	Hs.39635	ESTs
18861	2	F10452	Hs.12254	ESTs
24553	2	Z38521	Hs.9428	ESTs
19289	2	H16568	Hs.23748	ESTs
14185	2	AA490911	Hs.22393	Homo sapiens drp1 mRNA complete cds
30723	2	N51935	Hs.47374	EST
34031	2	AA192614	Hs.83577	Human LIM protein MLP mRNA complete cds
18434	2	AA232206	Hs.50743	ESTs
14647	2	D20378	Hs.30731	EST -

*FIG..7Ci*

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
41048	2	N92734	Hs.115985	ESTs
38157	2	AA486858	Hs.105702	EST
33299	2	W73790	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
16616	2	AA035446	Hs.61783	ESTs
3276	2	M93718	Hs.76983	Nitric oxide synthase 3 (endothelial cell)
33022	2	W46976	Hs.94667	EST
31704	2	N75055	Hs.14632	ESTs
38713	2	AA608577	Hs.112575	ESTs
20396	2	N48293	Hs.12296	ESTs
10310	2	R87373	Hs.75429	ESTs
22388	2	R63695	Hs.1432	Protein kinase C substrate 80K-H
15936	2	Z11737	Hs.2664	Flavin-containing monooxygenase 4
23667	2	T86826	Hs.142528	ESTs
30903	2	N57730	Hs.48058	EST
20938	2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]
5935	2	X62466	Hs.108338	CDW52 antigen (CAMPATH-1 antigen)
19304	2	H16976	Hs.7973	ESTs
8804	2	AB000463	Hs.16227	Homo sapiens mRNA for SH3 binding protein complete cds clone:RES4-23A
41485	2	R49689	Hs.5260	ESTs Weakly similar to C06G8.3 [C.elegans]
24685	2	Z39406	Hs.11797	ESTs Moderately similar to retinoid X receptor interacting protein [M.musculus]
25403	2	AA063316	Hs.104747	EST - RC: AA063316
35773	2	AA406219	ESTs	
27965	2	AA464267	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds
16911	2	AA058659	Hs.60669	ESTs

*FIG.-7Cj*

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
ACCESSION			
42315	2	T97353	EST - RC_T97353
40632	2	N45221	EST - RC_N45221
15722	2	W79046	Homo sapiens DBI-related protein mRNA complete cds
14842	2	T47519	EST - T47519
36088	2	AA417344	ESTs Moderately similar to located at OATL1 [H.sapiens]
15527	2	W28798	Phosphodiesterase 6A cGMP-specific rod alpha
10302	2	R84933	ESTs
21243	2	R08773	ESTs
7759	2	AA234687	ESTs Weakly similar to F59C6.4 [C.elegans]
		AA234687	ESTs Weakly similar to F59C6.4 [C.elegans]
		N74336	ESTs
31672	2	N74336	ESTs
26799	2	AA284722	ESTs
25857	2	AA156504	EST
16695	2	AA043115	ESTs Weakly similar to ORF YDL077c [S.cerevisiae]
964	2	HG1804-	EST - HG1804-HT1829
12439	2	AA401452	ESTs
19599	2	H41235	ESTs
24223	2	W70158	ESTs
21052	2	N93764	ESTs Very weakly similar to hypothetical protein [H.sapiens]
17463	2	AA121338	EST - RC_AA121338
28949	2	F03032	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]
34140	2	AA215637	ESTs
7465	2	AA120886	EST - /A120886
17376	2	AA102425	EST - RC_AA102425
5130	2	U79288	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Homo sapiens clone 24525 mRNA sequence
19684	2	H48488	ESTs
		HS.143798	ESTs

**FIG.-7CK**

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
8166	2	AA359093		EST - AA359093
19202	2	H11509	Hs.22482	ESTs
20439	2	N50785	Hs.13269	ESTs
10431	2	AA011310	Hs.3757	ESTs
29707	2	H98244	Hs.42519	ESTs
39868	2	H37909	Hs.107680	ESTs
8988	2	C00185	Hs.10444	ESTs
41350	2	R40442	Hs.75652	Glutathione S-transferase M5
13121	2	AA436156	Hs.110837	ESTs
15747	2	W88550	Hs.132188	ESTs
18674	2	F03989	Hs.18995	ESTs Weakly similar to KIAA0412 [H.sapiens]
914	2	HG1019-		EST - HG1019-HT1019
23804	2	T91086		EST - RC_T91086
26556	2	AA279089	Hs.88550	ESTs
8567	2	AA453381	Hs.104900	ESTs
30457	2	N47686	Hs.64607	Human RACH1 (RACH1) mRNA complete cds
21975	2	R45441	Hs.23710	ESTs
17452	2	AA120766	Hs.70724	ESTs
31958	2	N93495	Hs.54960	ESTs
31495	2	N69850	Hs.49759	ESTs
32490	2	T16389	Hs.81248	Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA complete cds
39174	2	AA621067	Hs.112944	ESTs
21572	2	R34073	Hs.69740	Zinc finger protein 136 (clone pHZ-20)
15914	2	Y09846	Hs.81972	V-ski avian sarcoma viral oncogene homolog
12014	2	AA281769	Hs.7214	Human Hpast (HPAST) mRNA complete cds

**FIG.-7C1**

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
9484	2	H50178	Hs.108081	ESTs Highly similar to PROTEIN PHOSPHATASE PP2A 55 KD REGULATORY SUBUNIT NEURONAL ISOFORM [Oryctolagus cuniculus]
			Hs.117619	ESTs
19147	2	H09751	Hs.124027	ESTs
36276	2	AA424179	Hs.57911	ESTs
16475	2	AA025903	Hs.20755	ESTs
21304	2	R11208	Hs.10024	ESTs
11199	2	AA176446	Hs.85564	ESTs
18093	2	AA187955	Hs.31040	EST
19190	2	H11274	EST - W76399	EST - W76399
15710	2	W776399	Hs.23540	ESTs
18707	2	F04627	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)
6477	2	X91504	Hs.15119	ESTs
20823	2	N68869	Hs.75649	EXTRACELLULAR SIGNAL-REGULATED KINASE 3
16336	2	AA018601	Hs.35104	ESTs
19680	2	H48457	Hs.19066	ESTs
24833	2	Z41087	Hs.109047	ESTs
24058	2	W23709	Hs.112272	ESTs
26180	2	AA251230	Hs.7765	ESTs
37177	2	AA447988	Hs.26054	ESTs
14047	2	AA482597	Hs.225552	ESTs
10770	2	AA058683	Hs.138805	ESTs
41994	2	T47601		

PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	UNIGENE ACCESSION CLUSTER	UNIGENE DESCRIPTOR
19217	2	H12243	EST - RC_H12243
36532	2	AA429889	Acrosin ESTs
23378	2	T60072	Hs.10688 ESTs
1450	2	J03071	Growth hormone 1 ESTs
8007	2	AA293072	Moderately similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]
		AA084723	EST - RC_AA084723
17266	2	Z40923	Hs.24812 ESTs
24819	2	X95325	DNA-BINDING PROTEIN A ESTs
6532	2	AA287651	Hs.86641 ESTs
26850	2	AA227523	Hs.108788 ESTs
34175	2	AA282169	EST - RC_AA282169 ESTs
34620	2	AA402495	Hs.77978 ESTs
27085	2	N24730	Hs.15420 ESTs
20173	2	AA129060	EST - RC_AA129060 Homo sajiens clone 24510 mRNA sequence
17574	2	R60920	Hs.26419 EST
22330	2	N29696	Hs.44076 ESTs
30070	2	N52322	Hs.19978 EST
20487	2	D83703	Peroxisomal biogenesis factor 6 Human RGP3 mRNA complete cds
724	2	U27655	Hs.82294 ESTs
4132	2	AA452705	Weakly similar to D2045.9 [C.elegans] EST
8557	2	W95626	Hs.23954 EST
33659	2	AA449716	Hs.59718 ESTs
13375	2	N57007	Hs.5723 EST
30891	2	AA480045	Hs.94074 EST
13988	2	R59906	Hs.7934 ESTs
22306	2		Hs.100530 ESTs

**FIG.-7Cn**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23167	2	T33164	Hs.12840	Homo sapiens germline mRNA sequence
20873	2	N70134	Hs.31476	ESTs
7231	2	AA059327	Hs.6580	Homo sapiens clone 23718 mRNA sequence
24582	2	Z38752	Hs.26330	ESTs
11320	2	AA213667	Hs.22222	ESTs
16388	2	AA020781	Hs.60847	ESTs
24608	2	Z38888	Hs.25046	Homo sapiens clone 23930 mRNA sequence
7809	2	AA248085	Hs.12469	ESTs
13163	2	AA437225	Hs.22410	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]
20549	2	N54991	Hs.37991	EST - HG3227-HT3404
1139	2	HG3227-AA401489		EST - RC_AA401489
35572	2	Z49105	Hs.137591	H.sapiens HD21 mRNA
6964	2	AA449704	Hs.77637	Homeo box A4
27704	2	W69725	Hs.10711	ESTs
33196	2	N59373	Hs.26812	ESTs
30963	2	AA476937	Hs.24441	ESTs Human mRNA for TPRD complete cds
13886	2	AA007509	Hs.75395	Homo sapiens mRNA for hoxA7 protein
16164	2	AA181926	Hs.70954	ESTs Moderately similar to RETROVIRUS-RELATED
18083	2	N21207	Hs.129942	POL POLYPROTEIN [Mus musculus]
20107	2	T16556	Hs.6653	ESTs
23004	2	AA011678	Hs.40470	ESTs
16238	2	AA195042	Hs.85978	ESTs
18189	2	AA457377		EST - RC_AA457377
37567	2			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
2174	2	L42611	Hs.111758	KERATIN TYPE II CYTOSKELETAL 6D
38958	2	AA609707	Hs.112751	ESTs
37919	2	AA478162	Hs.104965	ESTs
28905	2	D81123	Hs.57475	ESTs
33315	2	W74418	Hs.55410	ESTs
7421	2	AA095600		EST - AA095600
3745	2	U09117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds
19545	2	H37834	Hs.32699	ESTs
21204	2	R07632	Hs.17949	EST - AA428531
8416	2	AA428531		EST - RC_AA128926
17569	2	AA128926		
19572	2	H39195	Hs.22223	ESTs Highly similar to ALPHA-2-MACROGLOBULIN
22760	2	R93714	Hs.33833	PRECURSOR [Homo sapiens]
19354	2	H18829	Hs.121515	ESTs
40618	2	N39565	Hs.108540	ESTs
29913	2	N23708	Hs.43429	ESTs
22571	2	R78565	Hs.138395	EST
7598	2	AA174185	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds
25385	2	AA059099	Hs.109727	ESTs
14176	2	AA490620	Hs.11809	ESTs
37400	2	AA453578	Hs.120994	ESTs Weakly similar to T20D3.5 [C.elegans]
29487	2	H85120	Hs.80881	N-ACETYLGLUCOSAMINE SYNTHASE
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
322	2	D21241		EST - D21241_xpt1
22224	2	R55192	Hs.25689	ESTs
19488	2	H27675	Hs.25604	ESTs
10568	2	AA029703	Hs.36574	ESTs
10872	2	AA099357	Hs.15780	ESTs Moderately similar to ATP-BINDING CASSETTE TRANSFORTER 2 [Mus musculus]
29987	2	N26172	Hs.43760	ESTs
30799	2	N53143	Hs.64001	ESTs
9638	2	L07592	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds
21069	2	N98461	Hs.17706	ESTs
27195	2	AA411473	Hs.65311	ESTs
9241	2	D79565		EST - D79565
9218	2	D61469	Hs.56896	ESTs
22238	2	R55763	Hs.107287	ESTs
7512	2	AA136369		EST - AA136369
17438	2	AA115508	Hs.2780	Jun D proto-oncogene AFFX-HSAC07/X00351_M
24932	2	AFFX-F01525	Hs.3786	Glutamate receptor metabotropic 3
28911	2	AA125969	Hs.34769	ESTs Weakly similar to F35G12.9 [C.elegans]
10944	2	T98199	Hs.142702	ESTs
42324	2	AA287665	Hs.8245	ESTs
34756	2	AA421050	Hs.24545	ESTs
12743	2	R10075	Hs.14890	ESTs
21275	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2
13676	2	AA430474	Hs.16466	ESTs
13009				

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
7403	2	AA094921	Hs.79788	ESTs
11151	2	AA159961	Hs.25819	ESTs
35669	2	AA404707	Hs.54865	ESTs
17701	2	AA135941	Hs.71626	ESTs
18713	2	F04686	Hs.21782	ESTs
24144	2	W52312	Hs.30303	ESTs Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]
30741	2	N52175	Hs.22222	ESTs
23042	2	T23433	Hs.7105	ESTs
18479	2	AA233483	Hs.87159	ESTs
8314	2	AA410355	Hs.103081	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]
7990	2	AA291786	Hs.32822	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
10388	2	AA005355		EST - RC_AA005355
9407	2	H20086		EST - H20086
42791	2	AFFX-AA255470		AFFX-HIJMGAPDH/M33197_M
26302	2	N51924	Hs.88040	ESTs
30722	1	AFFX-AA609262	Hs.47370	ESTs
24965	1	AA461300	Hs.30643	ESTs
38850	1	Z30643	Hs.123123	H.sapiens mRNA for chloride channel (putative) 2139bp
13746	1	N68117	Hs.41119	ESTs
6893	1	AA152312	Hs.72047	ESTs
31403	1	AA033874	Hs.12035	ESTs
17830	1			
10583	1			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
20913	1	N72116	Hs.57435	Natural resistance-associated macrophage protein 2
35607	1	AA402267	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]
9920	1	NA44756	Hs.141935	ESTs Weakly similar to transformation-related protein [H.sapiens]
9468	1	H46074	Hs.31562	ESTs
29469	1	H82929		EST - RC_H82929
18121	1	AA191310	Hs.89608	Protein phosphatase 2 (formerly 2A) regulatory subunit A (PR 65) beta isoform
14705	1	D59362	Hs.6217	ESTs
18692	1	F04444	Hs.61557	EST
16543	1	AA029430	Hs.40763	ESTs
16359	1	AA019197	Hs.144550	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydroge
40818	1	N63772		ESTs
35205	1	AA398161	Hs.97602	ESTs Weakly similar to GOLIATH PROTEIN [Drosophila melanogaster]
7831	1	AA249175	Hs.96334	EST
17794	1	AA150260	Hs.72062	ESTs
11347	1	AA224245	Hs.26612	ESTs
17919	1	AA161125	Hs.72384	EST
22184	1	R53520	Hs.102755	ESTs
14827	1	T35288	Hs.90421	ESTs
28091	1	AA481788	Hs.87593	ESTs
28815	1	D59267	Hs.56782	ESTs
17813	1	AA151480	Hs.91202	ESTs
24655	1	Z39191	Hs.27262	ESTs Weakly similar to Lph17p [S.cerevisiae]

**FIG..7Cs**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
15611	1	W51743	Hs.35096	ESTs
39998	1	H62865	Hs.38132	ESTs
15700	1	W73859	Hs.78061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds
22045	1	R48965	Hs.24796	EST
36770	1	AA435753		EST - RC; AA435753
9877	1	N31127	Hs.40098	ESTs
22467	1	R68284	Hs.28399	ESTs
32400	1	R97176	Hs.110783	ESTs
10802	1	AA069425	Hs.20573	ESTs
23033	1	T17353	Hs.108894	Homo sapiens clone 23918 mRNA sequence
17593	1	AA129856		EST - RC; AA129856
14867	1	T58588	Hs.100419	ESTs
20266	1	N32118	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]
14447	1	AA609045	Hs.11759	ESTs
37994	1	AA479919		EST - RC; AA479919
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein
11970	1	AA280687	Hs.4069	ESTs
19738	1	H53059	Hs.15548	ESTs
14471	1	AA609346	Hs.20102	ESTs
14855	1	T54762	Hs.9786	ESTs
24725	1	Z39781	Hs.8004	Homo sapiens Duo mRNA complete cds
5796	1	X55019	Hs.99975	Cholinergic receptor nicotinic delta polypeptide
20259	1	N31598	Hs.12727	ESTs
18441	1	AA232508	Hs.77480	ESTs

**FIG.-7Ct**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
18468	1	AA233177	Hs.87134	ESTs
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]
8830	1	AB002319	Hs.8663	Human mRNA for KIAA0321 gene partial cds
15287	1	W07461	Hs.121559	ESTs Highly similar to DIPHTHINE SYNTHASE [Saccharomyces cerevisiae]
16477	1	AA026031	Hs.61312	ESTs
21969	1	R45334	Hs.21175	ESTs
22340	1	R61522	Hs.26892	ESTs
12884	1	AA426259		EST - RC_AA426259
8682	1	AA477891	Hs.104476	ESTs
22594	1	R79793	Hs.29900	ESTs
19131	1	H09331	Hs.122791	ESTs
17103	1	AA074997		EST - RC_AA074997
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]
35401	1	AA399593	Hs.97682	EST
10901	1	AA112307	Hs.25224	ESTs
19546	1	H37901	Hs.32706	ESTs
15378	1	W26448	Hs.15071	ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]
30292	1	N35978	Hs.82364	ESTs
39087	1	AA620607	Hs.111591	ESTs
37896	1	AA477463	Hs.77039	Ribosomal protein S28
8836	1	AB002325	Hs.105917	Human mRNA for KIAA0327 protein complete cds
16150	1	AA005428	Hs.60140	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
23955	1	T97467	Hs.18065	ESTs Weakly similar to alternatively spliced product using exon 13A [H.sapiens]
37812	1	AA469939	Hs.105323	ESTs
14782	1	S72370	Hs.89890	Pyruvate carboxylase
23540	1	T79178	Hs.14463	ESTs
41552	1	R59352	Hs.101253	Human mRNA for KIAA0296 gene complete cds
21836	1	R42569	Hs.22444	EST
11467	1	AA234089	Hs.14593	ESTs
18347	1	AA219230	Hs.86815	ESTs
8215	1	AA389673	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]
15505	1	W28366	Hs.7252	Homo sapiens clone 24800 mRNA sequence
22764	1	R93802	Hs.33687	ESTs
14966	1	U07620	Hs.89661	Human MAP kinase mRNA complete cds
24213	1	W69184	Hs.23973	ESTs
8165	1	AA358888	Hs.104135	Homo sapiens mRNA for DRIM protein
32724	1	T90750	Hs.15230	ESTs Weakly similar to F25H2.2 [C.elegans]
8212	1	AA386236	Hs.96757	Homo sapiens transcription factor SUPT3H (SUPT3H) mRNA complete cds
9834	1	M92299	Hs.22554	Homeo tox B5 (2.1 protein)
7229	1	AA059213	Hs.91898	ESTs
15649	1	W58725	Hs.75074	H.sapiens mRNA for MAP kinase activated protein kinase
42306	1	T96538	Hs.45090	Human K+ channel beta 1a subunit mRNA alternatively spliced complete cds
9159	1	D31483	Hs.90062	Homo sapiens clone 23565 unknown mRNA partial cds
20040	1	H96712	Hs.125198	ESTs
42218	1	T86444	Hs.110095	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
15526	1	W28790	Hs.81124	ESTs
17790	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]
17595	1	AA129929	Hs.71166	EST
31314	1	N66866	Hs.49278	EST
9777	1	M57888	Hs.95946	GRANZYME H PRECURSOR
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR
23547	1	T79448	Hs.14577	EST
12076	1	AA284362	Hs.6448	ESTs Weakly similar to No definition line found [C.elegans]
11956	1	AA279991	Hs.124691	ESTs
15391	1	W26651	Hs.15961	ESTs
9287	1	D82557	Hs.18104	ESTs
16419	1	AA022466	Hs.61141	EST
21713	1	R39930	Hs.21034	ESTs
12905	1	AA427537	Hs.32419	ESTs
30257	1	N34961	Hs.75873	H.sapiens mRNA for Zyxin
28134	1	AA487622	Hs.64095	ESTs
16380	1	AA019750	Hs.40797	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]
10553	1	AA028904	Hs.33215	ESTs
18063	1	AA180054	Hs.73677	ESTs
39820	1	H24085	Hs.25443	ESTs
7374	1	AA093378	Hs.101810	ESTs
13109	1	AA435838	Hs.7985	ESTs
19378	1	H19673	Hs.31670	ESTs
24325	1	W84733	Hs.3978	ESTs

**FIG.-7Cw**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22318	1	R60224	Hs.7065	ESTs
24249	1	W73069	Hs.12600	ESTs
16514	1	AA027946	Hs.44608	ESTs
21421	1	R21741	Hs.23258	ESTs Weakly similar to !!! ALU SUBFAMILY SQ WARNING
8397	1	AA426178	Hs.71725	ESTs Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]
8412	1	AA428090	Hs.26102	ESTs
10072	1	R14782	Hs.31931	ESTs
10349	1	AA001908	Hs.18160	ESTs
14492	1	AA609635	Hs.27497	EST - Tg2512
14930	1	T92512	X81001	Small includable cytokine A5 (RANTES)
15861	1	AA043800	Hs.141503	ESTs
16706	1	AA045643	Hs.62645	ESTs
16744	1	AA062980	Hs.62866	EST
16950	1	AA155779	Hs.66960	ESTs
17836	1		Hs.29759	ESTs Weakly similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]
18834	1	F10207	Hs.13269	ESTs
19178	1	H10992	Hs.100910	EST
19767	1	H54720	Hs.36941	ESTs
21341	1	R14959	Hs.21871	EST Moderately similar to ninein [M.musculus]
21466	1	R24518	Hs.23674	EST
21602	1	R36624	Hs.135137	ESTs
21748	1	R40697	Hs.21290	EST
21860	1	R43089		EST - RC_R43089
21891	1	R43590	Hs.13290	ESTs

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
21937	1	R44508	Hs.222653	ESTs
22006	1	R46244	Hs.23110	ESTs
22054	1	R49116	Hs.25067	EST
22222	1	R55042	Hs.106645	ESTs
22292	1	R59385	Hs.141053	Homo sapiens bestrophin (VMD2) mRNA alternatively spliced product complete cds
22383	1	R63463	Hs.23282	ESTs
22446	1	R67259	Hs.25968	EST
23103	1	T23939	Hs.7344	ESTs
23872	1	T94562	Hs.17338	EST
24291	1	W80642	Hs.16951	ESTs
24640	1	Z39086	Hs.21403	ESTs
27519	1	AA435835	Hs.90695	ESTs
32067	1	R06424	Hs.64896	ESTs
32204	1	R44210	Hs.91440	EST
32692	1	T79942	Hs.90930	ESTs
33714	1	Z39430	Hs.65749	ESTs
33733	1	Z39668	Hs.65792	ESTs
33873	1	AFFX-AFFX-DrapX-3	AFFX-DrapX-3	
35434	1	AA400034	Hs.97769	EST
35950	1	AA412498	Hs.104778	ESTs
36483	1	AA428865	Hs.98563	EST
36615	1	AA431469	Hs.98737	ESTs
37329	1	AA452138	Hs.3781	Homo sapiens BAC clone RG118D07 from 7q31
37700	1	AA461090	Hs.124826	EST
38285	1	AA489840	Hs.105302	ESTs

**FIG.\_7Cv**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
38887	1	AA609422	Hs.112705	EST
38933	1	AA609606	Hs.112732	ESTs
39894	1	H42037	Hs.144150	ESTs
40244	1	H91660	Hs.30250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds
40645	1	N47952	Hs.102624	EST
40819	1	N63787	Hs.109304	ESTs
41445	1	R45611	Hs.137696	ESTs Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]
41700	1	R85829	Hs.101883	EST
41776	1	T03170	Hs.100165	EST
13254	1	AA446587	Hs.6775	ESTs Highly similar to ALANINE AMINOTRANSFERASE [Homo sapiens]
8171	1	AA362708	Hs.5009	ESTs Weakly similar to mTERF [H.sapiens]
23030	1	T17291	Hs.6995	ESTs
8406	1	AA427510	Hs.104287	ESTs
16767	1	AA046650	Hs.40342	ESTs
25010	1	AA005315	Hs.51262	ESTs
14829	1	T35529		EST - T35529
34584	1	AA280934	Hs.132872	ESTs Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]
15909	1	Y07868	Hs.38842	H.sapiens mRNA for Pirin isolate 1
9922	1	N44971	Hs.107164	Spectrin beta non-erythrocytic 1
15381	1	W26496	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]
22168	1	R53024	Hs.25985	ESTs
11690	1	AA252762	Hs.31235	ESTs

**FIG.\_7Cz**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
22999	1	T16510	Hs.6624	ESTs
24490	1	Z38153	Hs.26921	ESTs
19993	1	H91255	Hs.15227	ESTs
19689	1	H48825	Hs.36291	ESTs
12450	1	AA401809	Hs.19865	ESTs
24368	1	W87280	Hs.124800	ESTs
22565	1	R77631	Hs.29126	ESTs
18872	1	F10542	Hs.12292	ESTs
15358	1	W26105	Hs.8961	ESTs
24186	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]
23863	1	T93870	Hs.17265	ESTs
23846	1	T93078	Hs.17117	EST
15143	1	U79257	Hs.86921	Human clone 23932 mRNA sequence
9711	1	L44334	Hs.10432	ESTs Weakly similar to BENOMYL/METHOTREXATE RESISTANCE PROTEIN [Candida albicans]
22544	1	R74235	Hs.80844	Homo sapiens mRNA for KIAA0573 protein partial cds
41506	1	R52088		EST - RC_R52088
39345	1	C21105	Hs.7768	Homo sapiens FGF-1 intracellular binding protein (FIBP) mRNA complete cds
22272	1	R58922	Hs.26590	ESTs
16434	1	AA024494	Hs.61199	ESTs
17255	1	AA084412		EST - RC_AA084412
22692	1	R88711	Hs.34183	ESTs
38830	1	AA609189	Hs.116415	ESTs
9179	1	D50312	Hs.102308	Human rRNA for uKATP-1 complete cds
42547	1	W73946		EST - RC_W73946

**FIG.-7Da**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
36195	1	AA421144	Hs.79592	EST - RC_AA421144
29355	1	H70121	Hs.104441	ESTs
34608	1	AA281765	Hs.16917	ESTs
20779	1	N67553	Hs.34274	ESTs
11081	1	AA149826	Hs.24642	ESTs
12151	1	AA291269	Hs.9899	EST - RC_H52379
39935	1	H52379	Hs.72146	ESTs
7157	1	AA037199	Hs.57732	ESTs
17858	1	AA156596	Hs.87068	Homo sapiens p38beta2 MAP kinase mRNA complete cds
34885	1	AA302831	R72597	EST - RC_R72597
18445	1	AA232648	Hs.12448	ESTs Weakly similar to unknown protein [H.sapiens]
22524	1	R72597	F09988	ESTs Weakly similar to unknown protein [H.sapiens]
19224	1	AA464689	Hs.5244	ESTs Weakly similar to unknown protein [H.sapiens]
18803	1	AA180352	Hs.23294	ESTs Weakly similar to weak similarity to HSP90 [C.elegans]
13810	1	AA164750	Hs.72733	ESTs
18070	1	AA620736	Hs.72499	ESTs
17937	1	R71892	Hs.112893	ESTs
39115	1	AA058555	Hs.25996	ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]
22517	1	AA497049	Hs.63392	ESTs
16906	1	T96407	Hs.32501	ESTs
14251	1	R06569	Hs.17812	ESTs
23923	1	AA131921	Hs.19721	ESTs
21177	1	H57725	Hs.71030	ESTs
25705	1		Hs.124031	ESTs
19805	1			

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
19668	1	H47656	Hs.33991	EST
36693	1	AA432389	Hs.98702	ESTs
14036	1	AA482107	Hs.5473	ESTs
20859	1	NG9825	Hs.16762	ESTs
23849	1	T93113		EST - RC_T93113
18265	1	AA207122	Hs.86316	ESTs
35275	1	AA398530	Hs.97363	ESTs
10262	1	R77869	Hs.110493	ESTs
21757	1	R40789	Hs.21299	ESTs
21541	1	R31607	Hs.24420	ESTs
16873	1	AA056258	Hs.63264	EST
19646	1	H46006	Hs.31677	ESTs
23719	1	T89160	Hs.138506	ESTs
19608	1	H41581	Hs.31582	ESTs Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]
17382	1	AA102731	Hs.109072	ESTs
16864	1	AA055971	Hs.63238	ESTs
10897	1	AA111881	Hs.9192	ESTs
17028	1	AA070178		EST - RC_AA070178
19220	1	H12318	Hs.24324	ESTs
9726	1	L44574	Hs.125235	ESTs
24570	0	Z38681	Hs.27150	ESTs
22167	0	R53021	Hs.25873	ESTs
42537	0	W73417	Hs.103183	EST
18806	0	F10005	Hs.12599	ESTs
16585	0	AA033948	Hs.4236	ESTs

**FIG.\_7Dc**

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PRIMARY KEY	FOLD DOWNREGULATED OF TUMOR vs.	ACCESSION	UNIGENE CLUSTER	UNIGENE DESCRIPTOR
17309	0	AA086232 R97419	Hs.68717 Hs.35718	EST Moderately similar to mariner transposase [H.sapiens] ESTs
22813	0	AA022953	Hs.61172	EST
16429	0	R46526	Hs.25377	EST
22013	0	AA431277	Hs.32419	ESTs
8439	0	T10042	Hs.4205	ESTs
22934	0	AA432386	Hs.1191	Human mRNA for KIAA0073 gene partial cds EST - R31745
13063	0	R31745		EST
10122	0	AA195263	Hs.86001	EST
18195	0	W72557	Hs.57836	ESTs
33249	0	AA063378	Hs.144270	ESTs
16966	0	AA223929	Hs.86902	EST
18363	0	AA219304	Hs.74561	ALPHA-2-MACROGLOBULIN PRECURSOR
34154	0	AA011210	Hs.95044	ESTs
16222	0	AA079306		EST - RC_AA079306
17174	0			

*FIG.-7Dd*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			UNIGENE ID	DESCRIPTION	
16074	>10	AA001507	ESTs	other	other
25047	>10	AA011031	ESTs	other	other
25082	>10	AA017257	ESTs	other	other
16490	>10	AA026418	ESTs	other	other
25179	>10	AA031268	H.sapiens mRNA for kinesin-2	other	other
25215	>10	AA035540	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other	other
25282	>10	AA044825	ESTs	other	other
16810	>10	AA053636	ESTs	SS,	other
16835	>10	AA054438	ESTs	other	other
10747	>10	AA055841	ESTs	other	other
10748	>10	AA055892	ESTs	other	other
16993	>10	AA065300	Human mRNA for KIAA0035 gene partial cds	TM	other
17051	>10	AA070801	ESTs	other	other
10840	>10	AA084104	ESTs	other	other
7296	>10	AA085661	ESTs	other	other
7325	>10	AA090842	ESTs	other	other
			Weakly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]		?
17419	>10	AA113349	EST	other	other
17541	>10	AA127459	ESTs	other	other
17559	>10	AA128407	ESTs	?	?
25669	>10	AA128978	ESTs	other	other
17600	>10	AA130596	ESTs	other	other
10992	>10	AA132523	Homo sapiens BAC clone RG119C02 from 7p15	TM	other
17654	>10	AA133250	ESTs	other	other
17734	>10	AA137246	ESTs	TM	other
25801	>10	AA148530	EST - RC_AA148530	EST	?
25806	>10	AA149007	EST	?	?

**FIG.-8Aa**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO	ORF
11121	>10	AA1156359 AA164289 AA164494	Human TAR DNA-binding protein-43 mRNA complete cds ESTs ESTs	?	other other	
11160	>10		Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H.sapiens]			
25925	>10		Human clone iota unknown protein mRNA complete cds ESTs	?	other TM other	
25934	>10	AA165355 AA169379 AA171895 AA173290	Homo sapiens clone 24749 and 24750 mRNA sequences Human HOXA1 mRNA long transcript and alternatively spliced forms complete cds		other	
17987	>10					
18008	>10					
33953	>10					
33980	>10	AA180223	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN EST - RC_AA190888		other	
34013	>10	AA190888 AA191348	ESTs	other	other	
34014	>10	AA191348	ESTs	other	TM	
34015	>10	AA191353	ESTs	other	other	
34070	>10	AA196549	ESTs	?	SS, other	
18260	>10	AA206801	ESTs	other	TM	
34105	>10	AA207123	ESTs	other	other	
34107	>10	AA209469	ESTs	other	TM	
18330	>10	AA216722	Human mRNA for apolipoprotein E receptor 2 complete cds Ribonuclease L (2'5'-oligo)soadenylate synthetase-dependent)	other	other	
18362	>10	AA223912	inhibitor			
18392	>10	AA227751	ESTs			
34188	>10	AA228030	ESTs			
34197	>10	AA232315	Homo sapiens clone 23797 and 23917 mRNA partial cds	other		
25948	>10	AA234365	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds	?		
25951	>10	AA234556				

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
11561	>10	AA236533	Evi-1		other
26059	>10	AA236685	ESTs		other
26100	>10	AA242835	Human mRNA for KIAA0391 gene complete cds		other
11603	>10	AA243052	ESTs Highlysimilar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]		other
7785	>10	AA243375	EST - AA243375		?
34372	>10	AA251973	ESTs	TM	?
26240	>10	AA252282	Human mRNA for KIAA0152 gene complete cds		other
34382	>10	AA252512	ESTs	other	?
34391	>10	AA252703	EST - RC_AA252703		?
26274	>10	AA253011	ESTs	other	?
34400	>10	AA253400	ESTs	other	?
26291	>10	AA253422	ESTs	other	?
26355	>10	AA256379	ESTs	other	?
11813	>10	AA258158	ESTs	other	?
34518	>10	AA278721	ESTs	other	?
26545	>10	AA278979	ESTs	other	?
26574	>10	AA279504	ESTs	other	?
34554	>10	AA280016	DNA polymerase gamma	TM	?
34561	>10	AA280298	ESTs	TM	?
26628	>10	AA280641	ESTs Highlysimilar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]	ESTs	other
11969	>10	AA280670	ESTs	SS, TM	
34575	>10	AA280738	ESTs	?	
26677	>10	AA281636	ESTs	?	
26700	>10	AA282197	EST		
34672	>10	AA284372	ESTs		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	STRUCTURAL	
34692	>10	AA285079	ESTs	other	
12143	>10	AA290991	ESTs	other	
8092	>10	AA316272	ESTs	TM	
34904	>10	AA321746	EST	other	
8111	>10	AA323787	ESTs	other	
8125	>10	AA330771	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM	
26916	>10	AA331393	ESTs	other	
26926	>10	AA342402	ESTs	other	
26935	>10	AA347193	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]	TM	
35038	>10	AA350541	ESTs Moderately similar to URACIL-DNA GLYCOSYLASE 1 PRECURSOR [H.sapiens]	TM	
35049	>10	AA350857	ESTs	other	
35106	>10	AA371561	EST Weakly similar to putative p150 [H.sapiens]	?	
35197	>10	AA398120	ESTs	other	
35277	>10	AA398536	ESTs	other	
35309	>10	AA398660	EST	other	
35322	>10	AA398710	H. sapiens RNA for CLCN3	TM	
27037	>10	AA400198	ESTs	TM	
35495	>10	AA400527	ESTs	?	
27046	>10	AA400670	Homo sapiens mRNA for < IAA0582 protein partial cds	other	
35500	>10	AA400715	ESTs	other	
12480	>10	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-Cyp) mRNA complete cds	other	
35693	>10	AA405485	ESTs Weakly similar to similar to complex testis-specific protein [C.elegans]	other	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ORF	
35697	>10	AA405512	Homo sapiens KIAA0431 mRNA partial cds	other	other
35766	>10	AA406169		other	other
35769	>10	AA406206		other	other
35798	>10	AA410231		other	other
35801	>10	AA410291		other	other
35803	>10	AA410295		other	other
35822	>10	AA411144		TM	?
35874	>10	AA412024		EST	?
35958	>10	AA412550		ESTs	TM
36052	>10	AA417027		EST	other
36258	>10	AA423962	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	ESTs	other
36288	>10	AA424502		other	?
36307	>10	AA424803		EST	?
36371	>10	AA426017		ESTs	TM
36395	>10	AA426353		other	other
36405	>10	AA426406	Homo sapiens mRNA for KIAA0530 protein partial cds	other	other
36506	>10	AA429610		SS,	other
36571	>10	AA430726		EST	?
36695	>10	AA433910		ESTs	?
36739	>10	AA435610		EST - RC_AA435610	other
36753	>10	AA435686		ESTs	?
36845	>10	AA436198		ESTs	SS, TM
13136	>10	AA436560		ESTs	SS,
13143	>10	AA436619		ESTs	other
36958	>10	AA442060		ESTs	?
36962	>10	AA442082		ESTs	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
36981	>10	AA442845 AA443971	EST ESTs	Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	?
13237	>10				other
13242	>10	AA445994 AA446131 AA446312	ESTs ESTs ESTs	Weakly similar to !!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]	other other other
37057	>10				
37068	>10				
37074	>10	AA446344 AA446486	ESTs Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds		SS, ?
37084	>10				
37135	>10	AA447540 AA447714 AA447772 AA449311	EST EST - RC_AA447714 ESTs Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds		?
37159	>10				other
37168	>10				?
37246	>10				other
37310	>10	AA4451707 AA454610 AA454632 AA454660 AA455248 AA456641 AA458864 AA458996	ESTs ESTs ESTs ESTs EST - RC_AA455248 ESTs ESTs Human signalling lymphocytic activation molecule (SLAM) mRNA complete cds		other ?
37453	>10				TM
37456	>10				?
27787	>10				other
37492	>10				TM
37546	>10				other
37601	>10				SS, TM
37611	>10				other
37615	>10	AA459101 AA460017	Human serine/threonine kinase mRNA partial cds ESTs		other other
37653	>10				

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			ORF		
37677	>10	AA460530	Homo sapiens orphan G protein-coupled receptor HG38	other	
			mRNA complete cds		
37777	>10	AA464860	Homo sapiens Jak2 kinase mRNA complete cds	other	
8648	>10	AA465016	Homo sapiens serine protease-like protease (nes1) mRNA complete cds	?	
37816	>10	AA469954	EST		
37829	>10	AA470084	ESTs	other	
28015	>10	AA477421	ESTs	other	
37978	>10	AA479294	EST - RC_AA479294	other	
37979	>10	AA479295	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]	other	
37983	>10	AA479348	H.sapiens mRNA for SYT	TM	
14054	>10	AA485223	ESTs	other	
38121	>10	AA485724	EST - RC_AA485724	other	
28122	>10	AA485928	ESTs Weakly similar to LOK [M.musculus]	other	
38167	>10	AA487207	EST - RC_AA487207	other	
38172	>10	AA487424	EST - RC_AA487424	other	
38179	>10	AA487492	Homo sapiens clone 235c2 mRNA sequence	other	
38182	>10	AA487501	ESTs	other	
38194	>10	AA487969	ESTs	?	
28141	>10	AA488432	ESTs	other	
38211	>10	AA488687	ESTs	other	
38235	>10	AA489030	ESTs	other	
38280	>10	AA489791	EST - RC_AA489791	other	
38316	>10	AA490500	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	other	
38330	>10	AA490882	ESTs	other	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	STRUCTURAL INFO	
38456	>10	AA504343	ESTs	SS, other	
38460	>10	AA504462	ESTs	other	
38553	>10	AA521471	ESTs	?	
38580	>10	AA598545	ESTs		
38590	>10	AA598648	Human mRNA for transcriptional activator hSNF2b complete cds	other	
38601	>10	AA598738	ESTs	?	
28323	>10	AA599639	ESTs	other	
38828	>10	AA609177	ESTs	TM	
38838	>10	AA609215	EST - RC_AA609215	?	
38867	>10	AA609318	Human cbl-b mRNA complete cds	TM	
38871	>10	AA609333	EST	?	
38970	>10	AA609749	ESTs	other	
38984	>10	AA609839	ESTs Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	?	
39045	>10	AA610077	ESTs	other	
39062	>10	AA620333	EST	?	
39080	>10	AA620552	EST - RC_AA620552_r	?	
39110	>10	AA620709	ESTs Weakly similar to HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II [C.elegans]	other	
39176	>10	AA621091	ESTs	other	
39218	>10	AA621330	ESTs	other	
39221	>10	AA621346	Homo sapiens protein phcsphatase with EF-hands-1 (PPEF-1) mRNA complete cds	other	
39232	>10	AA621409	ESTs	?	
21	>10	AB000905	H.sapiens histone H4 gene		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	UNIGENE DESCRIPTOR	
8963	>10	AFFX-HUMTFRR/M1150';_M	?	?	
33890	>10	AFFX-HUMTFRR/ M11507	AFFX-HUMTFRR/M1150';_5	?	
39302	>10	C14944	ESTs	other	?
39329	>10	C20797	EST	other	?
28644	>10	D12163	ESTs	other	
218	>10	D13540	PROTEIN-TYROSINE PHOSPHATASE 2C	other	
236	>10	D13645	Human mRNA for KIAA020 gene complete cds	other	
9127	>10	D30037	PHOSPHATIDYLINOSITOL	other	
459	>10	D38293	Human mRNA for clathrin-like protein complete cds	TM	
39405	>10	D50975	ESTs	other	
39433	>10	D52037	Human thymidine kinase 2 (TK2) mRNA complete cds	other	
39436	>10	D52692	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM	
14708	>10	D59388	EST	?	
39488	>10	D60831	ESTs	other	
39504	>10	D80632	ESTs	other	
765	>10	D86096	Prostaglandin E receptor 3 (subtype EP3) {alternative products}	?	
787	>10	D86969	Human mRNA for KIAA0215 gene complete cds	other	
789	>10	D86971	Human mRNA for KIAA0217 gene partial cds	other	
39529	>10	F02202	ESTs	?	
39535	>10	F02450	ESTs Moderately similar to unknown protein [H.sapiens]	TM	
18676	>10	F04022	ESTs	other	
18718	>10	F04915	ESTs	other	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		
			ESTs	ESTs	ORF STRUCTURAL INFO
18762	>10	F09458	ESTs	other	?
18782	>10	F09739	ESTs	other	?
29080	>10	F13655	ESTs	other	?
19001	>10	H02890	ESTs	other	?
19164	>10	H10395	EST	other	?
39725	>10	H11323	ESTs	other	?
19203	>10	H11593	ESTs	other	?
19328	>10	H17808	ESTs	other	?
19387	>10	H20128	ESTs	SS, ?	?
39787	>10	H20131	ESTs	other	?
19389	>10	H20165	EST	other	?
39832	>10	H26279	EST - RC_H26279	other	?
19591	>10	H40688	ESTs	other	?
29229	>10	H48459	Human mRNA for KIAA0186 gene complete cds	other	?
19727	>10	H52702	ESTs	other	?
19787	>10	H56679	ESTs	SS,TM	?
39995	>10	H62474	EST	TM	?
29331	>10	H68116	ESTs	?	?
29344	>10	H68839	EST	other	?
40064	>10	H72283	EST	other	?
40083	>10	H73466	ESTs	other	?
19949	>10	H78263	EST - RC_H88296	other	?
40204	>10	H88296	ESTs	Weakly similar to line-1 protein ORF2 [H.sapiens]	?
29523	>10	H88353	ESTs	?	?
29551	>10	H90134	ESTs	?	?
29645	>10	H95840	ESTs	?	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
20057	>10	H98079	ESTs	other	?
976	>10	HG2036-	EST - HG2036-HT2090	?	?
		HT2090			
1158	>10	HG3344-	EST - HG3344-HT3521	?	?
		HT3521			
1210	>10	HG37-HT37	EST - HG37-HT37	?	?
1346	>10	HG4716-	EST - HG4716-HT5158	?	?
		HT5158			
1349	>10	HG4747-	EST - HG4747-HT5195	?	?
		HT5195			
1445	>10	J03027	MHC class I protein HLA- $\beta$	?	?
1570	>10	K01383	EST - K01383	?	?
1684	>10	L07541	Replication factor C (activator 1) 3 (38kD)	other	TM
1852	>10	L17328	Human FEZ2 mRNA partial cds	?	?
1856	>10	L18920	MELANOMA-ASSOCIATED ANTIGEN 2	other	SS, TM
1863	>10	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	other	SS, TM
2070	>10	L37378	Homo sapiens guanylyl cyclase (RetGC-2) mRNA complete cds	other	SS,
2123	>10	L40396	Homo sapiens (clone s2271) mRNA fragment	other	other
2144	>10	L41349	Phospholipase C beta 4	other	other
9723	>10	L44542	ESTs	other	other
2188	>10	L47276	EST - L47276	other	other
2343	>10	M15353	Eukaryotic translation initiation factor 4E	other	TM
2627	>10	M29610	Glycophorin E	?	TM
2857	>10	M58597	Fucosyltransferase 4 (alpha (1,3) fucosyltransferase	myeloid-specific)	?
3021	>10	M68941	Protein tyrosine phosphatase non-receptor type 4	other	?
3163	>10	M84424	Cathepsin E		

**FIG.-8Ak**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
3196	>10	M86917	Oxysterol binding protein	other	
20088	>10	N20054	ESTs Weakly similar to putative p150 [H.sapiens]	?	
29795	>10	N20641	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE	other	
40427	>10	N21147	PROTEIN 3 [Homo sapiens]	other	
40444	>10	N22140	ESTs Highly similar to TUEULIN GAMMA CHAIN [Euploites octocarinatus]	other	
29893	>10	N23003	ESTs Homo sapiens citrate synthase mRNA complete cds	TM	
40498	>10	N26086	ESTs Homo sapiens citrate synthase mRNA complete cds	SS,	
40559	>10	N33024	ESTs Homo sapiens citrate synthase mRNA complete cds	SS,	
30190	>10	N33264	EST H.sapiens mRNA for diubiquitin	?	
30207	>10	N33920	EST H.sapiens clone 23915 mRNA sequence	other	
20304	>10	N34686	ESTs Homo sapiens clone 23915 mRNA sequence	?	
20307	>10	N34830	ESTs Homo sapiens clone 23915 mRNA sequence	other	
30265	>10	N35115	ESTs Homo sapiens clone 23915 mRNA sequence	other	
40594	>10	N35388	ESTs Homo sapiens KIAA0428 mRNA complete cds	other	
40604	>10	N38893	ESTs Homo sapiens KIAA0428 mRNA complete cds	other	
40631	>10	N45124	ESTs NUCLEAR FACTOR RIP140	?	
40660	>10	N49104	ESTs NUCLEAR FACTOR RIP140	?	
30610	>10	N50138	ESTs NUCLEAR FACTOR RIP140	?	
30617	>10	N50646	ESTs NUCLEAR FACTOR RIP140	?	
30631	>10	N50807	ESTs NUCLEAR FACTOR RIP140	?	
30790	>10	N52935	ESTs NUCLEAR FACTOR RIP140	?	
20564	>10	N55443	ESTs NUCLEAR FACTOR RIP140	?	
40760	>10	N57927	ESTs NUCLEAR FACTOR RIP140	?	
30938	>10	N58561	ESTs NUCLEAR FACTOR RIP140	?	
20614	>10	N59230	ESTs NUCLEAR FACTOR RIP140	?	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR		ORF STRUCTURAL INFO
			UNIGENE ID	DESCRIPTION	
20657	>10	N62889	ESTs		other
31136	>10	N63512	ESTs	Weakly similar to MC1F1.4 [C.elegans]	TM
40827	>10	N64051	ESTs	Homo sapiens Wemer syndrome gene complete cds	other
31310	>10	N66831	EST	?	?
40876	>10	N67607	Human Rho-associated coiled-coil containing protein kinase p160ROCK mRNA complete cds	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds	other
20791	>10	N68057	ESTs	H.sapiens mRNA for orphan nuclear hormone receptor	other
40905	>10	N68738	ESTs		other
40911	>10	N69114	ESTs		other
40913	>10	N69218	ESTs		other
31484	>10	N69466	ESTs		other
31619	>10	N73449	ESTs		other
41005	>10	N79516	ESTs		TM
31818	>10	N89774	ESTs	Homo sapiens mRNA for KIAA0292 gene partial cds	other
31872	>10	N91109	EST		other
41040	>10	N91948	ESTs		other
31944	>10	N93193	ESTs		other
41065	>10	N93618	ESTs		other
32034	>10	N98926	ESTs	Moderately similar to DMR_N9 PROTEIN [H.sapiens]	other
41107	>10	R01634	ESTs		other
41163	>10	R08176	ESTs		other
21238	>10	R08564	ESTs	Plasminogen-like protein	other
21240	>10	R08613	ESTs		other
21412	>10	R20670	ESTs		other
21519	>10	R27975	EST - RC_R27975		other
41381	>10	R42278	H.sapiens mRNA for TRE5		?

**FIG.-8Am**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR	ORF STRUCTURAL INFO	
				TM	other
32189	>10	R43183	ESTs	?	?
32195	>10	R43471	ESTs Weakly similar to ORF YOR258w [S.cerevisiae]	TM	?
21902	>10	R43822	EST	?	?
21946	>10	R44707	ESTs	?	?
22072	>10	R49406	ESTs	?	?
32240	>10	R50976	Ribonuclease L (2'5'-oligo)adenylate synthetase-dependent inhibitor	other	other
32258	>10	R55623	ESTs	other	other
22258	>10	R56432	ESTs	other	other
22282	>10	R59197	ESTs	other	other
32277	>10	R61493	Human mRNA for rod photoreceptor protein complete cds	other	other
22372	>10	R62831	EST	?	?
22400	>10	R64109	ESTs	other	other
41593	>10	R64129	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE	other	other
10233	>10	R71427	ESTs ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]	other	other
41654	>10	R76437	THROMBOXANE-A SYNTHASE	TM	other
22557	>10	R76722	ESTs	other	other
22576	>10	R79111	ESTs	?	?
22593	>10	R79777	EST	?	?
41678	>10	R80675	EST	other	other
41719	>10	R89260	EST - RC_R89260	other	other
22793	>10	R96208	ESTs	other	other
41752	>10	R97063	ESTs	other	other
3375	>10	S50223	HKR-T1	other	other
3406	>10	S66896	SQUAMOUS CELL CARCINOMA ANTIGEN 1	other	other
3522	>10	S80267	Spleen tyrosine kinase	other	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE DESCRIPTOR	
41793	>10	T03887	ESTs	?	
23198	>10	T40530	ESTs	other	
23360	>10	T58531	ESTs	other	
32635	>10	T61116	ESTs	other	
42177	>10	T79786	ESTs	?	
23623	>10	T84047	ESTs	?	
23662	>10	T86674	ESTs	other	
42242	>10	T89579	Homo sapiens E2F-related transcription factor (DP-1) mRNA complete cds	other	
23759	>10	T90313	ESTs	other	
23832	>10	T92018	ESTs	other	
32740	>10	T92950	ESTs	?	
42290	>10	T95105	ESTs	SS,TM other	
3598	>10	U01157	Glucagon-like peptide-1 receptor		
3659	>10	U04313	Protease inhibitor 5 (maspin)		
3799	>10	U10690	Human MAGE-5a antigen (MAGE5a) gene complete cds		
3870	>10	U14518	Centromere protein A (17kD)		
3913	>10	U16261	Human MDA-7 (mda-7) rr RNA complete cds		
4029	>10	U21090	Human DNA polymerase delta, small subunit mRNA complete cds		
4157	>10	U28811	Human cysteine-rich fibroblast growth factor receptor (CFR-1)		
4178	>10	U30246	mRNA complete cds	TM	
15006	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1)	TM	
4193	>10	U31116	mRNA complete cds	TM	
4306	>10	U36798	Human beta-sarcoglycan A3b mRNA complete cds	TM	
			Homo sapiens platelet cG1-PDE mRNA complete cds		

**FIG.\_8Ao**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				?	?
4362	>10	U39817	Bloom syndrome	other	other
4386	>10	U40622	DNA repair protein XRCC4	other	other
4388	>10	U40714	Human tyrosyl-tRNA synthetase mRNA complete cds.	other	other
4455	>10	U43944	MALATE OXIDOREDUCTASE	other	other
4477	>10	U45880	Human IAP-like protein ILP mRNA complete cds	other	other
4680	>10	U55766	Human Rev interacting protein Rip-1 mRNA complete cds	TM	other
4702	>10	U57341	EST - U57341	other	other
4713	>10	U57721	Human L-kynurenine hydrolase mRNA complete cds	other	other
4787	>10	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds	other	other
4862	>10	U65437	Human homeodomain-containing protein (HANF) mRNA complete cds	?	?
4945	>10	U69108	Homo sapiens mRNA for TRAF5 complete cds	other	other
4975	>10	U71088	Human MEK5 mRNA complete cds	other	other
4994	>10	U72514	Human C2f mRNA complete cds	other	other
5002	>10	U72761	Human karyopherin beta 3 mRNA complete cds	other	other
5021	>10	U73524	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds	TM	other
5149	>10	U79716	Human reelin (RELN) mRNA complete cds	SS,	?
5214	>10	U83303	H.sapiens mRNA for granulocyte chemotactic protein	?	?
5243	>10	U85946	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds	other	other
32789	>10	W02779	ESTs Moderately similar to kinesin-73 [D.melanogaster]	other	other
42354	>10	W19346	ESTs	other	other
42390	>10	W40150	Homo sapiens chromosome-associated polypeptide (HCAP)	other	other
33006	>10	W46286	mRNA complete cds	TM	other
			ESTs Weakly similar to Zk.1058.5 [C.elegans]		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
33020	>10	W46891	ESTs Weakly similar to polypeptide N-acetyl/galactosaminyltransferase [H.sapiens]	other	
33109	>10	W59961	Human mRNA for KIAA0389 gene complete cds	other	
24197	>10	W67277	ESTs	other	
24215	>10	W69425	ESTs	other	
33301	>10	W73883	ESTs Weakly similar to rholetkin [M.musculus]	other	
33343	>10	W79834	ESTs Weakly similar to F46B6.7 [C.elegans]	other	
33377	>10	W81219	ESTs	other	
42602	>10	W86423	Murine leukemia viral (bmi-1) oncogene homolog	other	
33556	>10	W90705	Protease inhibitor 5 (maspin)	other	
33616	>10	W93726	ESTs	TM	
33666	>10	W95876	Cell division cycle 2 G1 to S and G2 to M	?	
5510	>10	X05360	Wingless-type MMTV integration site 2 human homolog	SS,	
5558	>10	X07876	Teratocarcinoma-derived growth factor 1	TM	
5603	>10	X14253	HISTONE H2A.X	SS,	
5619	>10	X14850	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	?	
5623	>10	X14975	G1 to S phase transition 1	other	
5692	>10	X17644	Matrix metalloproteinase 1 (interstitial collagenase)	other	
5789	>10	X54925	Aspartyl/glucosaminidase	SS,	
5799	>10	X55330	CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1	?	
5802	>10	X55544	Human mRNA for adipogenesis inhibitory factor	other	
5857	>10	X58377	ATPase Ca++ transporting plasma membrane 2	TM	
5960	>10	X63575	(NOTE: redefinition of symbol)	SS,TM	
5963	>10	X63629	Cadherin 3 (P-cadherin)	?	
5986	>10	X64810	Protein convertase subtilisin/kexin type 1	other	
6041	>10	X67155	MITOTIC KINESIN-LIKE PROTEIN-1		

**FIG.-8Aq**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO	ORF
			UNIGENE DESCRIPTOR	STRUCTURAL INFO		
6095	>10	X69962	Fragile X mental retardation 1	other		
6106	>10	X70683	SRY (sex determining region Y)-box 4	TM		
6155	>10	X74331	DNA primase polypeptide 2A (58kD)	other		
6167	>10	X74987	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other		
6188	>10	X76029	NEUROMEDIN U-25 PRECURSOR	TM		
6315	>10	X81889	H.sapiens mRNA for p0071 protein	other		
6382	>10	X85133	H.sapiens RBQ-1 mRNA	other		
6384	>10	X85137	Human kinesin-like spindle protein HKSP (HKSP)	other		
			mRNA complete cds			
6438	>10	X89398	URACIL-DNA GLYCOSYLASE 1 PRECURSOR	?		
6449	>10	X89986	H.sapiens mRNA for NBK apoptotic inducer protein	TM		
6478	>10	X91648	H.sapiens mRNA for pur epsilon extended 3'untranslated region	SS,TM		
6479	>10	X91653	EST - X91653	?		
6494	>10	X92689	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase	TM		
			EST - Y08564	?		
6713	>10	Y08564	Homo sapiens importin-alpha homolog (SRP1gamma)	other		
6790	>10	Y12394	mRNA complete cds			
			EST - YEL003w/	?		
			YEL019c/	?		
			MMS21			
24915	>10	YEL003w/	ESTS			
42773	>10	YEL019c/	ESTS			
		MMS21	ESTS			
24545	>10	Z38462	ESTS			
33713	>10	Z39427	ESTS			
33791	>10	Z40883	ESTS			
42766	>10	Z99394	Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]	other		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
21558	>10	R33112	Human AF-6 mRNA complete cds		other ?
26718	>10	AA282576	ESTs		?
40113	9.9955090946	H78003	ESTs		other
10801	9.9879448276	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C.elegans]		?
37491	9.9513600842	AA455239	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]		other
23900	9.9272347693	T95789	ESTs Human mRNA for KIAA0101 gene complete cds		other
254	9.9198395324	D14657	ESTs Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)		other
6885	9.8970927914	Z29331	ESTs		SS, other
29693	9.8850766398	H97819	ESTs		?
26482	9.8765189024	AA262491	ESTs		other
23123	9.8699502035	T25306	ESTs		other
26525	9.8160399123	AA278392	ESTs Homo sapiens mRNA for high mobility group protein HMG2a		other
13110	9.7643356605	AA435840	EST Phosphoribosylglycinamide formyltransferase		other
34863	9.7087597628	AA2999784	EST Phosphoribosylaminomimidazole synthetase		?
39432	9.7034550083	D51691	ESTS Weakly similar to !!! ALU CLASS B WARNING		other
31312	9.6513325388	N66845	ENTRY !!! [H.sapiens]		?
21112	9.6358446349	R01179	ESTs		other
31572	9.6254820695	N71294	ESTs		?
17903	9.6221229759	AA160259	EST		other
20747	9.6094813734	N66842	ESTs		TM
4676	9.589223908	U55206	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	TM
34363	9.5627081023	AA251587	Homo sapiens mRNA for KIAA0530 protein partial cds	other	other
39094	9.540768988	AA620636		other	?
3888	9.5372000133	U15128	Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?	?
39386	9.506250529	D12184	ESTs	TM	other
7674	9.4458059039	AA203742	ESTs	TM	other
4192	9.4329744134	U31099	Human DP prostanoid receptor (PTGDR) mRNA partial cds	TM	TM
4507	9.422674945	U47050	Human putative calcium influx channel (htrp3) mRNA complete cds	TM	TM
35606	9.412026255	AA402227	ESTs Moderately similar to N-tropomodulin [R.norvegicus] Human nuclear factor I-B $\zeta$ (NFIB2) mRNA complete cds	other	?
4970	9.3649551013	U70862		?	?
19829	9.3432151573	H58813	EST	TM	?
14837	9.2878584141	T40145	ESTs	other	other
17336	9.2822148675	AA099585	ESTs	other	other
40541	9.2532836505	N30160	ESTs	?	?
29496	9.2487643833	H85434	EST	TM	?
29943	9.1797074262	N24786	ESTs Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	TM	TM
17997	9.1629681314	AA169633	EST	other	other
21320	9.1243463318	R11673	ESTs	other	other
13883	9.1178796537	AA476917	ESTs Weakly similar to Nc definition line found [C.elegans]	other	other
30539	9.0886887776	N49072	ESTs	other	?
32778	9.08777919549	W02063	EST	?	?
26380	9.0809559378	AA257012	EST	other	other
15888	9.0595893607	X95632	Human Abl interactor 2 (Abi-2) mRNA complete cds	other	other
40812	9.0012874244	N63419		other	other
903	8.9640387908	D90070	ATL-derived PMA-responsive (APR) peptide	other	other

**FIG.-8At**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR	ORF STRUCTURAL INFO	
				TM	other
22674	8.9515777733	R87160	ESTs	TM	other
40807	8.9510132281	N62995	TRANSCRIPTION INITIATION FACTOR IIF BETA SUBUNIT	TM	other
15244	8.9195644974	W00904	ESTs	TM	other
32296	8.8658776567	R67075	Zinc finger protein X-linked	TM	other
18269	8.8575656769	AA209467	ESTs	other	other
19662	8.8507626284	H47391	ESTs	other	other
41607	8.833925517	R67868	CLEAVAGE SIGNAL-1 PROTEIN	TM	other
2548	8.8299864699	M25897	Platelet factor 4	TM	other
7736	8.8279341243	AA232121	Human tyrosyl-tRNA synthetase mRNA complete cds	other	other
34490	8.7844537272	AA262354	ESTs	other	other
38658	8.7669313482	AA599477	ESTs	other	other
7528	8.765157554	AA149543	ESTs	other	other
39939	8.7555031142	H53454	EST - RC_H53454	other	other
25111	8.7232692309	AA020787	ESTs	?	?
21655	8.716167279	R38239	ESTs Highly similar to NADH-UBIQUINONE OXIDO	other	other
39663	8.665982852	H04756	REDUCTASE B17 SUBUNIT [Bos taurus]	?	?
1042	8.652112324	HG2510-HT2606	EST - HG2510-HT2606	?	?
32330	8.6361115426	R77776	ESTs	other	other
25382	8.6239456487	AA059007	ESTs	SS,	other
27074	8.5900813076	AA401475	ESTs Weakly similar to Cx6B1.3 [C.elegans]	other	other
3955	8.5298909183	U18259	MHC class II transactivator	other	other
4959	8.52646827	U70322	Human transportin (TRN) mRNA complete cds	?	?
2315	8.5259185808	M14123	EST - M14123_xpt1	other	other
37253	8.4896914632	AA449357	ESTs	?	?
39624	8.471316877	F10836	ESTs	?	?

*FIG.\_8Au*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			ESTs	Connective tissue activation peptide III	
23213	8.4569920887	T40891	ESTs	Connective tissue activation peptide III	?
2798	8.455596435	M54995	ESTs	?	TM
41154	8.4413390141	R07499	ESTs	other	?
32479	8.4093689549	T16282	ESTs	other	other
41251	8.3587565415	R28279	ESTs	other	other
19081	8.3583603183	H06701	ESTs	other	other
21098	8.3105927559	R00545	ESTs	other	other
14723	8.3061679053	D59894	ESTs	other	other
37154	8.2994822341	AA447666	ESTs	other	other
8068	8.2835586361	AA313387	ESTs	other	other
7485	8.281679348	AA129547	ESTs		
16501	8.2517969834	AA026969	ESTs		
34527	8.2419163754	AA279091	ESTs		
6700	8.1948675662	Y07867	ESTs		
2852	8.1928816537	M58460	ESTs		
11188	8.1862492468	AA172372	ESTs		
42293	8.183311064	T95333	ESTs		
5443	8.1763317544	X02530	ESTs	Interferon (gamma)-induced cell line protein 10 from	SS, TM
40937	8.1534810594	N70607	ESTs		?
23371	8.1499496068	T59505	EST - RC_T59505		other
26272	8.1339974519	AA252981	ESTs	Weakly similar to K07C11.10 gene product [C.elegans]	other
17306	8.1332403762	AA086201	ESTs		other
18497	8.1192326373	AA233795	ESTs		other
235	8.0944363901	D13644	ESTs	Human mRNA for KIAA0019 gene complete cds	TM
24525	8.0860187097	Z38347	ESTs		

**FIG.-8Av**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				TM	other
7826	8.0750029554	AA248884	EST - AA248884	TM	other
32142	8.0739258775	R38715	Homo sapiens clone 24540 mRNA sequence	ESTs	other
39067	8.0557768803	AA620405		ESTs	other
6235	8.0448957236	X78416	Casein alpha S1	ESTs	TM
29517	8.0017588725	H88261		ESTs	other
28570	7.9852455973	C21104	Homo sapiens STAT-induced STAT inhibitor-2 mRNA complete cds	ESTs	other
39344	7.9162087762	C21034	ESTs Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]	ESTs	other
18951	7.9002189759	H00580		ESTs	other
18953	7.8709160227	H00615		ESTs	other
18376	7.8564099916	AA226925		ESTs	other
19830	7.847878447	H58911		ESTs	other
36023	7.840835828	AA416881		ESTs	other
13347	7.8344414518	AA449238		ESTs	other
36614	7.8284591351	AA431466		ESTs	other
2192	7.8254072032	L48211	Homo Sapiens angiotensin II receptor gene complete cds	ESTs	?
33016	7.8006574068	W46577	H.sapiens mRNA for ESM-1 protein	ESTs	other
17215	7.7941954038	AA083044		ESTs	other
34894	7.7659738105	AA311881		EST	?
40614	7.695001222	N39257		ESTs	other
36295	7.6834749899	AA424534		ESTs	other
19564	7.6744302788	H38833		ESTs	TM
16914	7.6686405336	AA058665		ESTs	SS,
35967	7.6378079107	AA412694	Human splicing factor SRp55-2 (SRp55) mRNA complete cds	ESTs	other
21672	7.6364823402	R38635		ESTs	other
19918	7.6303275831	H69787		ESTs	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	ORF STRUCTURAL INFO	
				?	SS, other
10511	7.6297744492	AA024482	ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 [Homo sapiens]	ESTs	?
17721	7.6057911016	AA136590		EST	SS,
42302	7.6031859697	T96130		EST	other
26134	7.6000619383	AA243763		ESTs	other
18766	7.5621799008	F09497		ESTs	other
34492	7.501590494	AA262439	ATL-derived PMA-responsive (APR) peptide	EST - D14822	other
270	7.4512152125	D14822		ESTs	other
35975	7.4177746986	AA412738		ESTs	other
29842	7.4095809671	N21688		ESTs	other
35389	7.3913043319	AA399555		ESTs	other
19979	7.3868157166	H88477		ESTs	other
5793	7.3865864025	X54942	CDC28 protein kinase 2	EST - RC_H87770	other
19978	7.380969715	H87770		EST - RC_H87770	other
1280	7.3691089318	HG4126- HT4396		EST - HG4126-HT4396	?
31571	7.3676263454	N71250		ESTs	?
23765	7.3541191734	T90443	Weakly similar to KIAA0376 [H.sapiens]	ESTs	?
35123	7.3397933455	AA380927		EST	other
38252	7.3341119467	AA489247		ESTs	other
38216	7.3282021037	AA488861		ESTs	?
29418	7.2489407005	H77915	EST - RC_H77915	Human mRNA expressed in HC/HCC livers and Molt-4	other
4834	7.1980951054	U63541	proliferating cells partial sequence	ESTs	
42504	7.1913036522	W69803		ESTs	
6111	7.158000198	X71125	H.sapiens mRNA for glutamine cyclotransferase	TM	
41773	7.154479618	T03024	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]	other	

**FIG.-8Ax**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	ESTs
9951	7.1363626365	N71513	ESTs	other	other
28109	7.0941968224	AA485212	ESTs	other	?
988	7.0783044659	HG2160-HT2230	EST - HG2160-HT2230	TM	TM
29848	7.0610668511	N22107	ESTs	other	?
30628	7.0607950168	N50744	ESTs	other	?
22567	7.0225726353	R77771	ESTs	TM	TM
9347	7.006323071	H03686	ESTs	other	?
11696	7.0026773299	AA252894	ESTs	?	?
40584	7.0010096333	N34870	EST	TM	?
193	6.9767029188	D10923	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74	other	?
18305	6.9740536051	AA214048	Collagen type IV alpha 4	other	?
6078	6.9699682397	X69141	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	other	?
26741	6.902658703	AA283198	ESTs	other	?
35069	6.8992865685	AA358397	EST	other	?
23504	6.8977135983	T71042	ESTs	other	?
299	6.8824513029	D16815	Homo sapiens orphan nuclear hormone receptor BD73 mRNA 3' end	other	?
40583	6.88689903023	N34855	ESTs	other	?
31428	6.8623762224	N68594	ESTs	other	?
6169	6.8606959727	X75091	SET PROTEIN	other	?
39524	6.8567355171	F01905	MALATE OXIDOREDUCTASE	other	?
34578	6.8430689439	AA280837	ESTs	other	?
38678	6.837527995	AA599920	Small inducible cytokine A5 (RANTES)	other	?
23936	6.8251471804	T96930	ESTs	other	?
9326	6.8181321394	D89377	Msh (Drosophila) homeo tox homolog 2	TM	?
19188	6.8067351968	H11255	ESTs Highly similar to ACTIN-LIKE PROTEIN [Bos taurus]	TM	?

**FIG.-8AY**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				UNIGENE	EST
18185	6.7882148811	AA194983	Homo sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds	other	
27028	6.757529124	AA399630	ESTs Weakly similar to KIAA0371 [H.sapiens]	other	
41289	6.7519531681	R37265	EST	other	
34511	6.7364448798	AA278298	EST - RC_AA278298	?	
1566	6.7056207716	J05614	EST - J05614	?	
25675	6.6692299748	AA129757	ESTs Highly similar to 603 RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other	
5814	6.6584342828	X56088	CYTOCHROME P450 VII	SS, other	
13861	6.6236291607	AA470145	ESTs	other	
29794	6.6026313352	N20598	ESTs	other	
39333	6.5902382643	C20910	Cyclin B1	other	
3770	6.5835303599	U09609	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	other	
31831	6.5829933764	N89894	ESTs	?	
33063	6.5808125026	W53000	Homo sapiens clone 24431 mRNA sequence	other	
20326	6.5640084836	N35583	ESTs Weakly similar to PFI0BABLE E5 PROTEIN [Human papillomavirus type 58]	?	
34384	6.5535703492	AA252537	ESTs	other	
25599	6.5490481991	AA114091	Human (clone 8B1) Br-cathelin mRNA complete cds	other	
39749	6.5369363254	H14988	ESTs	other	
42596	6.5200567072	W85900	ESTs	?	
39606	6.5119482185	F10243	ESTs Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]	?	
14617	6.5105504748	C14983	ESTs	other	
27831	6.45670814	AA456044	ESTs	?	
34896	6.4496517783	AA312551	EST	?	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO	ORF
			UNIGENE	DESCRIPTOR		
27360	6.4434305006	AA425356	ESTs		other	
20126	6.4326610424	N22015	ESTs		TM	
6663	6.4324809977	Y00291	RETINOIC ACID RECEPTOR BETA-2		TM	
30692	6.4196636207	N51563	ESTs		other	
36472	6.4189542265	AA428633	EST		?	
9578	6.3961788753	H87652	Homo sapiens bicaudal-D (BICD) mRNA complete cds		other	
39670	6.3818496159	H05626	ESTs		other	
22697	6.3652792447	R89218	ESTs		other	
37308	6.3647804993	AA451694	EST		TM	
16101	6.3517262802	AA002147	EST		?	
20629	6.3486854401	N59798	ESTs		other	
36100	6.3364146287	AA411740	ESTs		other	
15488	6.3252590241	W28097	Homo sapiens clone 23711 unknown mRNA partial cds		other	
36667	6.3131273544	AA432136	ESTs		?	
30766	6.3115037924	N52627	EST - RC_N52627		?	
32882	6.2745311453	W37683	ESTs		TM	
18072	6.2675797205	AA180448	EST		?	
18231	6.2652604863	AA199747	Human mRNA for KIAA0096 gene partial cds		other	
38282	6.2514165678	AA489814	EST		?	
28125	6.250317021	AA486073	ESTs		other	
37464	6.2484456382	AA454747	ESTs		?	
36618	6.1946328223	AA431478	ESTs		other	
5082	6.1931116815	U78524	Human Gu binding protein mRNA partial cds		other	
1441	6.1777287039	J02963	Integrin alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex antigen CD41B)		other	
42105	6.14875944	T67710	ESTs		?	
6061	6.1394863141	X68314	Glutathione peroxidase 2 (gastrointestinal	SS,		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
32570	6.1156028796	T30222	ESTs	Weakly similar to tetracycline transporter-like protein [M.musculus]	TM
32504	6.1019612076	T17063	EST		?
23335	6.0977927504	T56804	EST		?
10867	6.0970991075	AA088458	ESTs	Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
30883	6.0911993489	N56923	EST		?
14528	6.0859008453	AA620295	ESTs		TM
29454	6.0685955036	H81308	EST		?
6798	6.0539173278	Y13153	Homo sapiens mRNA for lysozyme 3-monooxygenase		TM
21248	6.0525426545	R08871	ESTs		?
21940	6.0499964138	R44538	ESTs		?
29066	6.04555247653	F10927	Homo sapiens clone 23636 mRNA sequence		other
18774	6.0446826953	F09609	ESTs		?
36722	6.0172343991	AA435512	ESTs		SS,
18062	6.0034342969	AA179845	ESTs	Moderately similar to rabkinasin-6 [M.musculus]	other
22989	5.9992817406	T16305	ESTs		other
41745	5.9905623898	R95895	ESTs		?
8787	5.9894877658	AA504307	X-LINKED HELICASE II		other
20550	5.984861795	N55013	ESTs		other
26470	5.9417764101	AA262179	ESTs		other
16574	5.9356497569	AA031926	EST		other
693	5.9169537385	D80007	Human mRNA for KIAA0135 gene partial cds		other
4093	5.914830973	U25182	Human antioxidant enzyme AOE37-2 mRNA complete cds		TM
1192	5.9086264407	HG3546-HT3744	EST - HG3546-HT3744		?
22956	5.8954735623	T10248	ESTs		other

**FIG.\_8Bb**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			POLY A	ORF	
36723	5.891606409	AA435524	EST	?	other
2114	5.8844986595	L40384	EST - L40384	?	other
26872	5.868238789	AA291137	ESTs	?	other
6602	5.8663883018	X98266	EST - X98266_cds2	?	other
42701	5.8594493433	Z38612	ESTs	?	other
28573	5.84591116	C21118	ESTs	?	other
18290	5.8189427595	AA211901	ESTs	?	other
732	5.8043917941	D83781	Human mRNA for KIAA0197 gene partial cds	?	other
5330	5.8014145611	U91327	EST - U91327	?	other
33503	5.7990715189	W88720	EST	?	other
2553	5.7797050864	M26167	Human platelet factor 4 variation 1 (PF4var1) gene complete cds	?	other
34705	5.7658806254	AA286907	ESTs Weakly similar to putative p150 [H.sapiens]	?	other
42665	5.7594091043	W93659	ESTs	?	other
38180	5.7539310793	AA487495	EST - RC_AA487495	?	other
4244	5.7476738809	U33286	Human chromosome segregation gene homolog CAS mRNA complete cds	?	other
32822	5.7418957453	W16834	ESTs	?	other
3977	5.7245885557	U18991	Retinal pigment epithelium-specific protein (65kD)	?	other
24673	5.7202366155	Z39301	ESTs	?	other
6928	5.7120261128	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)	?	TM
38726	5.7030796258	AA608733	ESTs	?	other
39290	5.6892372058	C14573	Human mRNA for KIAA0029 gene partial cds	?	other
11405	5.6818873796	AA232231	ESTs	?	other
22538	5.6792006591	R73567	Homo sapiens meltrin-L precursor (ADAM12) mRNA complete cds	?	TM

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		TM
			STRUCTURAL INFO	ORF	
40747	5.6605393208	N56872	Homo sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds	ESTs	?
31596	5.6554024604	N72094		ESTs	other
6329	5.6415652518	X82279		EST - X82279	?
31578	5.6273323661	N71361		ESTs	other
33207	5.6271818482	W70051	H.sapiens mRNA for M-phase phosphoprotein mpp9		other
2545	5.6105860146	M25753	Cyclin B1	ESTs	other
22580	5.5988402647	R79156		ESTs	other
33592	5.5935314518	W93127		ESTs	other
28843	5.5734698755	D60252		ESTs	other
6160	5.5689050619	X74794	CDC21 HOMOLOG	ESTs	other
37987	5.5613456667	AA479666		ESTs	other
42515	5.5217868611	W72116	Homo sapiens clone 236:2 mRNA sequence		other
4732	5.5130668527	U58522	Human huntingtin interacting protein (HIP2) mRNA complete cds		other
3299	5.5099850678	M95623	Hydroxymethylbilane synthase		?
28320	5.473406981	AA599574		ESTs	?
746	5.471260899	D84454	Human mRNA for UDP-galactose translocator complete cds		TM
39373	5.4635804954	C21517		ESTs	other
3117	5.4398413537	M81182	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)		other
21257	5.4343612441	R09196	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]	ESTs	other
31487	5.4318648859	N69507		ESTs	other
28954	5.4137130511	F03153		ESTs	other
38928	5.389782721	AA609595		ESTs	other
29903	5.3722320622	N23366		EST	?
30925	5.3437432315	N58295	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE- HOMOLOG [H.sapiens]		?

**FIG.\_8Bd**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	STRUCTURAL INFO	
19091	5.3344615669	H07864	ESTs	TM	
28209	5.3138951918	AA491250	ESTs	other	
9470	5.3118897984	H46617	EST - H46617	other	
9435	5.3070056656	H30201	EST - H30201	?	
28552	5.2954432572	C20914	ESTs	other	
27411	5.2940164267	AA428137	ESTs	other	
30615	5.2924125264	N50556	ESTs	other	
28313	5.2657977167	AA599309	ESTs	TM	
39321	5.2649035384	C20632	ESTs	?	
29934	5.2531047395	N24194	ESTs	other	
1094	5.2496703122	HG2846-	EST - HG2846-HT2983	?	
		HT2983			
39578	5.2481126384	F08925	ESTs	TM	
11232	5.2466798424	AA186804	ESTs	other	
2466	5.2426349328	M21539	Human small proline rich protein (spril) mRNA clone 1292	other	
26843	5.2387758661	AA287450	ESTs	?	
40331	5.2353385567	H97562	ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 [Sepia officinalis]	other	
			EST - AA305116	other	
8035	5.205798365	AA305116	ESTs Weakly similar to weak similarity to procollagen alpha	other	
29793	5.1955425722	N20593	chain 1(V) chain [C.elegans]	other	
			EST	?	
34109	5.1481590107	AA210722	ESTs Weakly similar to ROSA26AS [M.musculus]	other	
26408	5.1432577257	AA258177	ESTs	TM	
19263	5.1427029807	H15054	ESTs	other	
24596	5.1416089352	Z38810	ESTs	other	
28589	5.1365059753	C21245	H.sapiens mRNA for apoptosis specific protein	other	
5684	5.1121931412	X17098	Pregnancy-specific beta-1 glycoprotein 6	other	

**FIG.-8Be**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
30710	5.1079347344	N51761	EST		?
35765	5.0973514948	AA406167	EST		?
26360	5.0863127861	AA256460	ESTs		?
2351	5.0849612092	M15796	Proliferating cell nuclear antigen		?
30262	5.0836877534	N35065	Homo sapiens clone 247:9 mRNA sequence	other	?
41792	5.0737512465	T03886	ESTs	other	?
36710	5.0703839864	AA434411	ESTs	other	TM
39090	5.0546885407	AA620628	ESTs	?	?
42185	5.0539926381	T79951	ESTs	?	?
18745	5.0460321557	F09134	ESTs	?	?
35746	5.0396841996	AA406063	ESTs	?	?
35356	5.0354809581	AA3999053	EST	?	?
36769	5.0312706878	AA435750	EST	?	?
36900	5.0279911548	AA436866	H.sapiens mRNA for M-phase phosphoprotein mpp9	other	?
27595	5.0244757301	AA443328	ESTs	?	?
16290	5.005611904	AA016145	ESTs	?	?
27117	5.0016146599	AA405098	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]	other	?
4304	4.9951954397	U36764	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit	other	?
33458	4.9907402071	W86835	Homo sapiens mRNA for KIAA0636 protein complete cds	other	?
26693	4.9800090679	AA282120	EST	?	?
12669	4.9758138651	AA417030	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other	?
29701	4.9708526387	H97970	EST	?	?
20480	4.9557253636	N52168	ESTs	TM	?
8720	4.9439110602	AA481218	EST - AA481218	other	?
34828	4.9431269475	AA292436	Homo sapiens semaphorin F homolog mRNA complete cds	SS,TM	?

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				?	?
14985	4.9416221032	U15128	Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2)	?	?
16115	4.9377553522	AA004420	gene complete cds	ESTs	other
42506	4.9348587118	W70074		EST	other
34761	4.9316837445	AA287833		ESTs	TM
11870	4.9281056201	AA262587		ESTs	other
23211	4.9258391854	T40889	Homo sapiens mRNA for KIAA0584 protein partial cds	ESTs	other
40611	4.9160502275	N39138	Homo sapiens putative RNA binding protein KOC (koc) mRNA	ESTs	other
42611	4.9128605354	W87006	complete cds	ESTs	other
39652	4.9045174605	H03099		ESTs	?
17581	4.889674751	AA129395		EST	?
37239	4.8704375389	AA449121		ESTs	other
18712	4.8703618781	F04677		ESTs	other
30709	4.8611171953	N51752	Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]	ESTs	other
34179	4.8503613948	AA227903	Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	ESTs	other
21433	4.825670988	R22183		EST	?
39731	4.8186142741	H11760		ESTs	other
31295	4.8116614607	N66653		ESTs	other
24647	4.804163055	Z39108		EST	?
31292	4.8008871817	N66615		ESTs	other
1285	4.7997542393	HG4157-HT4427		EST - HG4157-HT4427	?
1106	4.7932425858	HT4427		EST - HG2981-HT3127	?

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**ORF  
STRUCTURAL  
INFO**

<b>PRIMARY KEY</b>	<b>FOLD UPREGULATED OF TUMOR OVER NORMAL COLON</b>	<b>ACCESSION</b>	<b>UNIGENE DESCRIPTOR</b>	
			<b>STRUCTURAL INFO</b>	<b>UNIGENE DESCRIPTOR</b>
18212	4.7912262565	AA196506	ESTs	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3)
34367	4.782207045	AA251758	mRNA complete cds	other other
34802	4.7797760205	AA291468	ESTs	TM
34762	4.7775301546	AA287834	ESTs	other
11595	4.7696612848	AA242819	ESTs	other
8295	4.7639839111	AA405082	ESTs	?
17622	4.758635576	AA131584	ESTs	other
35781	4.7572463523	AA406335	ESTs	other
34754	4.7483874972	AA287642	ESTs	other
23237	4.7444854356	T47291	EST	?
37667	4.7280445357	AA460318	ESTs	other
11568	4.7257189975	AA236786	ESTs	other
38622	4.7190695733	AA598967	ESTs	?
5137	4.7057359474	U79296	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) CDC28 protein kinase 2	other
25038	4.7002244728	AA010065	ESTs	other
19288	4.7000147312	H16567	Collagen type I alpha-2	other
32503	4.6979488292	T17045	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT	TM
3278	4.6953739298	M94055	Integral transmembrane protein 1	TM
9696	4.6942061018	L38961	Homo sapiens putative DNA methyltransferase (DNMT2)	other
35400	4.6901390898	AA399591	mRNA complete cds	?
35246	4.6862691303	AA398367	EST Weakly similar to HS>60 protein [M.musculus]	other
36387	4.6822499271	AA426270	ESTs	other

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ORF	STRUCTURAL INFO
21509	4.6730072542	R27314	ESTs	other	
31381	4.6729672124	N67889	ESTs	other	
26723	4.6727894925	AA282781	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]	other	
36326	4.6703621086	AA425151	Human GAP SH3 binding protein mRNA complete cds	other	
17409	4.6688418667	AA113136	EST - RC_AA113136	other	
4908	4.65552339935	U67156	Human mitogen-activated kinase kinase 5 (MAPKK5) mRNA complete cds	other	
30594	4.6496238328	N49967	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE	other	
38286	4.64639735	AA489847	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]	?	
13073	4.6426509459	AA433950	ESTs	other	
40435	4.6240181066	N21614	Homo sapiens basic-leucine zipper transcription factor MafG (MAFG) mRNA complete cds	other	
14474	4.6228694379	AA609427	ESTs Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]	other	
38213	4.615309907	AA488847	ESTs Weakly similar to putative p150 [H.sapiens]	?	
5312	4.606644198	U90716	Human cell surface protein HCAR mRNA complete cds	SS,TM	
24225	4.6041550359	W70326	ESTs	?	
35588	4.5868982366	AA401750	EST	?	
29739	4.5863199051	H99626	EST	?	
7203	4.5792992577	AA053096	EST - AA053096	other	
2157	4.5772055869	L41939	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	SS,TM	
32086	4.5661024279	R11510	ESTs	?	
8085	4.5648114738	AA314779	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]	SS,	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
224	4.5622018989	D13633	Human mRNA for KIAA0008 gene complete cds		other
34006	4.5609980241	AA188761	DNA polymerase gamma		other
33656	4.5557384389	W95477	ESTs		other
34065	4.5537335124	AA195517	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]		TM
6028	4.5357922097	X66503	Adenylosuccinate synthase		other
4166	4.5032930671	U29463	Cytochrome B561		?
40262	4.5024727522	H93562	ESTs		TM
22687	4.5018672549	R88209	ESTs		TM
41069	4.4977510482	N93969	H.sapiens mRNA for hFat protein		SS,
8264	4.4793100575	AA401334	ESTs		other
27588	4.472017297	AA443187	ESTs		other
35882	4.4717597552	AA412047	ESTs		?
34479	4.465519191	AA262080	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1)		TM
15921	4.4548516436	Y12065	mRNA complete cds		
11279	4.4380038671	AA195399	Homo sapiens mRNA for nuclear protein hNop56		?
39222	4.4367650786	AA621348	ESTs		other
			ESTs Highly similar to DCYLICHL-PHOSPHATE BETA-		other
			GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]		other
34428	4.4364736766	AA256526	ESTs		other
8771	4.432067373	AA491188	ESTs		other
22193	4.4189610024	R53891	Homo sapiens mRNA from chromosome 5q21-22 clone:A3-A		other
7898	4.4066170674	AA263032	ESTs		other
19902	4.3886145805	H66736	ESTs		other
9276	4.3868095209	D82374	ESTs		other
10716	4.3794529068	AA053319	ESTs		TM

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE DESCRIPTOR	ORF	
13193	4.3751913512	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocitetus auratus]	?	other
5690	4.3723059417	X17620	NUCLEOSIDE DIPHOSPHATE KINASE A	?	other
35102	4.37147138	AA371509	EST - RC_AA371509	?	TM
17983	4.3612985467	AA169226	ESTs	?	other
24962	4.3497206925	AFFX-HUMTFR/M1150';_5	AFFX-HUMTFR/M1150';_5	?	?
31680	4.3416539669	N74438	ESTs	?	other
27168	4.330306894	AA410258	ESTs	?	other
28731	4.3231846659	D20981	EST	?	?
28348	4.3212284906	AA608752	ESTs	?	other
16335	4.3019861487	AA018587	ESTs Weakly similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]	?	?
33036	4.2915644973	W48580	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]	?	other
30180	4.2897721925	N33144	ESTs	?	SS,
35591	4.2895541242	AA401758	ESTs Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	?	SS,
25340	4.2721717135	AA054554	EST	?	TM
28106	4.2659103748	AA485084	ESTs	?	other
38690	4.2649184307	AA600121	ESTs	?	other
20203	4.2626499431	N26855	ESTs Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	?	other
10251	4.2608760694	R76185	ESTs Weakly similar to CC1H6.7 [C.elegans]	SS,	SS,
12684	4.2604192389	AA417558	ESTs	?	TM
31636	4.2509469427	N73680	Natural resistance-associated macrophage protein 2	?	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		UNIGENE DESCRIPTOR	STRUCTURAL INFO
			FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION		
20769	4.2479765348	N67277	ESTs	EST - K01884	other	?
1572	4.2353281083	K01884	ESTs	EST - K01884	other	other
10923	4.2292322072	AA116036	ESTs	ESTs	other	other
34380	4.2283792392	AA252414	ESTs	EST - R35733	other	other
10132	4.2222816115	R35733	ESTs	EST - R35733	other	other
16629	4.2161752119	AA036811	ESTs	ESTs	?	?
25146	4.1969683794	AA026356	ESTs	ESTs Moderately similar to !!! ALU SUBFAMILY SQ	other	other
28730	4.1965943098	D20959	ESTs	WARNING ENTRY !!! [H.sapiens]	other	other
10200	4.1874912391	R64521	ESTs	ESTs	other	other
38695	4.1545794663	AA600176	ESTs	ESTs	other	other
31365	4.150549979	N67550	ESTs	ESTs	other	other
42379	4.1496120668	W37999	ESTs	ESTs	other	other
28050	4.1428703354	AA479139	ESTs	Acid phosphatase 1 soluble	other	other
2620	4.1386565707	M29474	ESTs	Human recombination activating protein (RAG-1) gene	?	?
8927	4.1340593744	AF008442	ESTs	complete cds	other	other
13379	4.1269549188	AA449741	ESTs	Homo sapiens RNA polymerase I subunit hRPA39 mRNA	complete cds	complete cds
5134	4.1218251808	U79293	ESTs	Weakly similar to AF-9 PROTEIN [H.sapiens]	ESTs	ESTs
2626	4.1213948	M29581	ESTs	Human clone 23948 mRNA sequence	ESTs	ESTs
38005	4.1160483666	AA479969	ESTs	Zinc finger protein 8 (clone HF.18)	ESTs	ESTs
36575	4.1127196584	AA431085	EST	?	?	?
18296	4.1121837207	AA213620	ESTs	Weakly similar to putative p150 [H.sapiens]	ESTs	ESTs
29531	4.1111459313	H88953	ESTs	EST - RC_H88953	TM	TM

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ORF	?
143	4.1095880506	AFFX-HUMTFR/M11507_5			
10970	4.0967613396	M11507		other	
25836	4.0952825397	AA129390	ESTs	SS, ?	
19735	4.0937927853	AA152305	Interferon (gamma)-induced cell line protein 10 from EST	other	
40711	4.0909709431	H53038	ESTs	TM	
4149	4.0901471427	N53564	RAG (recombination activating gene) cohort 1	other	
5767	4.0862784557	U28386	MULTIFUNCTIONAL PRoteIN ADE2	SS,	
5503	4.0861035825	X53793	Stromelysin	other	
20310	4.0641711656	X05232	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN	SS,	
456	4.0599824566	N34893	B0280.9 IN CHROMOSOME III [Caenorhabditis elegans]	other	
7814	4.0559685576	D38145	Prostaglandin I2 (prostacyclin) synthase	SS,	
40230	4.0447282719	AA248406	ESTs	other	
33651	4.039204804	H90161	ESTs	SS,	
16777	4.0231657929	W95409	ESTs	other	
19110	4.0094905222	AA046968	EST	?	
34442	4.0077010365	H08778	ESTs	other	
5099	4.004992433	AA258093	HKR-T1	other	
8209	3.9990473163	U79247	Human clone 23599 mRNA sequence	TM	
24408	3.9976586074	AA384220	ESTs	other	
26596	3.9974919787	W90146	ESTs	other	
16485	3.9811264008	AA279943	Spleen focus forming virus: (SFV) proviral integration	other	
32969	3.9804901745	AA026269	oncogene spi <sup>1</sup>	ESTs	
27006	3.9799768093	W42451	ESTs	TM	
		AA398695	Weakly similar to E04F6.2 gene product [C.elegans]	other	

**FIG.- 8Bm**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				?	?
29809	3.9526765967	N21043	EST	TM	?
9596	3.9440163451	H91564	ESTs	other	?
29024	3.9377933938	F09315	Homo sapiens mRNA for KIAA0583 protein partial cds	other	?
21694	3.9356365584	R39317	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2)	other	?
			mRNA complete cds		
13207	3.929998104	AA443321	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-	other	?
37865	3.9143752629	AA476623	TERMINAL HYDROLASE C13A11.04C	other	?
			[Schizosaccharomyces pombe]		
36201	3.9129828172	AA421164	ESTs	?	?
8961	3.8981160269	AFFX-HUMTFR/M11507_3	AFFX-HUMTFR/M11507		
17444	3.8927133917	AA115933	ESTs	other	?
25869	3.8919834527	AA157267	ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN	TM	?
			ZK686.3 IN CHROMOSOME II [Caenorhabditis elegans]		
24862	3.89042252	Z41415	ESTs Highly similar to BCNE MORPHOGENETIC PROTEIN	other	?
			1 PRECURSOR [Mus musculus]		
26685	3.889363206	AA281950	ESTs	?	?
42300	3.8850230366	T95850	ESTs	other	?
6495	3.8830844863	X92715	Zinc finger protein 74 (Cox52)	TM	?
38604	3.8828045942	AA599803	ESTs	other	?
36358	3.8826713718	AA425756	ESTs	other	?
30560	3.873276445	N49284	MYB PROTO-ONCOGENE PROTEIN	other	?
14413	3.8724466158	AA600150	ESTs	other	?
23823	3.8574824967	T91805	Homo sapiens mRNA for ST1C2 complete cds	other	?
38158	3.853096838	AA487021	EST	?	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	STRUCTURAL	
2572	3.8519747554	M27281	Vascular endothelial growth factor	other	other
40100	3.8464168967	H75933	Laminin receptor (2H5 epitope)	ESTs	TM
40258	3.8462992993	H93340		ESTs	other
20944	3.8461621525	N74443		ESTs	other
20411	3.8459400966	N48963	Homo sapiens mRNA for KIAA0689 protein partial cds	ESTs	other
10345	3.8457714481	AA001663		ESTs	other
31261	3.8451974374	N66248		EST	other
8513	3.8378410994	AA446990		ESTs	other
13877	3.8363409835	AA476604		ESTs	other
40748	3.8253562321	N56879		EST	?
14509	3.8152852193	AA609943		ESTs	other
10281	3.8065567331	R80333		ESTs	other
25284	3.8044158642	AA045074	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H.sapiens]	ESTs	other
6730	3.7900025129	Y09305	H.sapiens mRNA for protein kinase Dyrk4 partial	ESTs	other
16033	3.7884592402	AFFX-HUMISGF3A/M97E35_MB	AFFX-HUMISGF3A/M97E35_MB	ESTs	?
		M97935	HUMISGF3A/		
39242	3.7827164808	AA621523		ESTs	other
27354	3.7794760435	AA425221		ESTs	?
4552	3.777263605	U49188	Human placenta (Diff33) mRNA complete cds	ESTs	SS,TM
18385	3.7756199108	AA227219	Homo sapiens CAGF9 mRNA partial cds	EST - RC_AA046067	other
16754	3.7677416053	AA046067		ESTs	other
12752	3.7671137403	AA421250		ESTs	other
42463	3.7601033106	W60180		ESTs	?
10614	3.7581669016	AA037357		ESTs	other
867	3.7459337969	D87716	Human mRNA for KIAA0007 gene partial cds	ESTs	other
7608	3.7336047135	AA180967		ESTs	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTS	EST - RC_AA399453
31795	3.732738742	N80703	ESTS	other	?
35377	3.7273784603	AA399453	EST - RC_AA399453	?	other
22828	3.7243928524	R98192	ESTS	other	other
25240	3.7243198336	AA0399713	ESTS	other	?
11008	3.7197361366	AA134289	ESTS Weakly similar to ASiH1 [D.melanogaster]	?	other
4341	3.7162349944	U38545	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLC1) mRNA complete cds	?	other
28833	3.7147818393	D59787	EST - RC_D59787_f	?	SS,
3750	3.7121007154	U09279	Collagen type XIX alpha 1	TM	TM
17483	3.6943413512	AA122147	ESTs	TM	TM
16854	3.6915208471	AA055552	ESTs Weakly similar to KIAA0319 [H.sapiens]	other	other
3709	3.6891656771	U07550	Heat shock 10 kD protein 1 (chaperonin 10)	?	?
1608	3.6652978422	L00205	KERATIN TYPE II CYTOSKELETON 6D	TM	TM
24577	3.6617721053	Z38727	Homo sapiens mRNA for KIAA0555 protein complete cds	other	other
31032	3.6570916386	N62508	ESTs	other	other
4951	3.6536195433	U69546	Homo RNA binding protein Etr-3 mRNA complete cds	other	other
37660	3.6523275307	AA460225	ESTs	?	?
20418	3.6495357091	N49209	ESTs	other	other
27995	3.6485167436	AA470155	Homo sapiens coatomer protein (COPA) mRNA complete cds	other	other
7971	3.6434397185	AA287423	ESTs	other	other
27606	3.64303453	AA443793	ESTs	other	other
24677	3.6427250633	Z39338	ESTs Highly similar to PCLOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]	TM	other
11070	3.6406198277	AA148521	ESTs Weakly similar to putative p150 [H.sapiens]	other	other
9328	3.6356048599	D89618	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds	other	other
36826	3.634689802	AA435996	ESTs	?	?

**FIG.-8Bp**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR	STRUCTURAL INFO	
				ORF	STRUCTURAL INFO
17678	3.6300045795	AA134275	Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3	other	
36209	3.6274694477	AA421266	ESTs Weakly similar to LIS-1 protein [H.sapiens]	?	
34120	3.6258090412	AA211615	EST	TM	
38152	3.6246442011	AA486737	H.sapiens mRNA for Sm protein F	TM	
38463	3.6184693268	AA504491	ESTs Weakly similar to contains similarity to C3HC4-class zinc finger [C.elegans]	TM	
20064	3.6183699978	H98653	ESTs	TM	
31256	3.59992620732	N66152	EST	?	
9713	3.5985228843	L44338	Homo sapiens mRNA for KIAA0525 protein-partial cds	other	
28622	3.5768056147	D11837	ESTs	?	
38057	3.5736105703	AA481549	EST - RC_AA481549	other	
28763	3.5688723791	D45568	EST	?	
16996	3.5680705709	AA069038	EST - RC_AA069038	TM	
28628	3.5604144617	D11888	ESTs Moderately similar to PROHIBITIN [H.sapiens]	?	
25804	3.5442954572	AA148885	ESTs	?	
2492	3.5423964239	M22898	Tumor protein p53 (Li-Fraumeni syndrome)	?	
14904	3.5411970737	T83389	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]	other	
25265	3.5347588502	AA043765	H.sapiens RY-1 mRNA for putative nucleic acid binding protein	other	
13606	3.5327912417	AA456437	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]	other	
42307	3.5318436465	T96595	EST - RC_T96595	TM	
1544	3.526202414	J05068	TRANSCOBALAMIN I PRECURSOR	SS,	
42339	3.5195061035	W02072	ESTs Weakly similar to Nc definition line found [C.elegans]	other	
42311	3.5183719631	T97257	ESTs	other	
2023	3.5040279423	L34600	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR	other	
4540	3.4955308569	U48807	Human MAP kinase phosphatase (MKP-2) mRNA complete cds	other	

**FIG.\_8Bq**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR	STRUCTURAL INFO	
				ORF	other
33707	3.4888534277	Z39297	Neuronal pentraxin II	SS,	
17220	3.4755763461	AA083070	EST - RC_AA083070_S	other	
24332	3.4725273806	W85782	ESTs	other	
35887	3.4668063718	AA412067	ESTs	other	
20158	3.4538150055	N23638	ESTs Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]	other	
8338	3.4465832071	AA417152	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other	
387	3.4421427234	D28589	EST - D28589	SS, TM	
12319	3.4356289717	AA398109	ESTs	TM	
38276	3.4313139432	AA489711	ESTs	other	
15643	3.4312194246	W58247	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]	TM	
11218	3.4232932843	AA180488	ESTs	?	
16539	3.417886379	AA029328	Human mRNA for KIAA0073 gene partial cds	other	
29203	3.4162847487	H28581	ESTs	other	
13838	3.4162403464	AA465342	ESTs	other	
25585	3.4160353003	AA112389	H4(D10S170)	SS,	
34018	3.4145338583	AA191488	Human high-affinity copper uptake protein (hCTR1) mRNA complete cds	TM	
251	3.4006042851	D14520	Basic transcription element binding protein 2	other	
3778	3.4004516201	U09848	Zinc finger protein 139 (clone pHZ-37)	other	
24535	3.3964397637	Z38409	ESTs	other	
16858	3.3925194041	AA055759	Human mRNA for KIAA012B gene partial cds	TM	
16127	3.3921645927	AA004669	ESTs	other	
36683	3.3841316491	AA432268	ESTs	other	
26149	3.3809497785	AA250824	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]	other	

**FIG.-8Br**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
4011	3.3798093471	U20536	Human cysteine protease Mch2 isoform alpha (Mch2)	mRNA complete cds	other
41001	3.3794250205	N78844	ESTs		other
5660	3.3789336731	X16396	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	ESTs	SS, SS,
19204	3.3776332343	H11629	ESTs		other
42323	3.3768515979	T98152	Fibrillin 2	ESTs	SS,
26928	3.3725378868	AA342580	ESTs		SS,
20497	3.369285912	N52565	ESTs		other
19226	3.36674249	H12455	ESTs		other
36267	3.3606641838	AA424046	ESTs		other
32257	3.3559796018	R54726	DNA-REPAIR PROTEIN X:RCC1	ESTs	other
17365	3.3522214732	AA101551	ESTs		other
15296	3.3491193196	W16684	Moderately similar to Similar to <i>S.cerevisiae</i> hypothetical protein L3111 [H.sapiens]	ESTs	other
17675	3.3485870272	AA134064	ESTs		other
40332	3.3456469589	H97565	Homo sapiens mRNA from chromosome 5q21-22 clone:A3-A	ESTs	?
7219	3.3385684843	AA056319	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A)	ESTs	other
			mRNA complete cds	ESTs	other
10006	3.3322827922	N81193	Homo sapiens mRNA for KIAA0628 protein complete cds	ESTs	?
33985	3.3276877441	AA181580	Homo sapiens importin beta subunit mRNA complete cds	ESTs	other
9570	3.3263855302	H85169	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3)	ESTs	other
			gene complete cds	ESTs	?
37551	3.3155406577	AA456679	ESTs		other
886	3.3111782759	D88613	Human mRNA for hGCMa complete cds	ESTs	other
23650	3.3069426629	T86293	ESTs		other
18367	3.3007433533	AA224180	ESTs	Moderately similar to ovarian-specific protein [R.norvegicus]	?

**FIG.-8Bs**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENIE DESCRIPTOR	ORF STRUCTURAL INFO
42494	3.2908070546	W69385	H.sapiens NuMA gene (Clone T33)	other
14310	3.2753564661	AA598412	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION [Saccharomyces cerevisiae]	SS, TM
19233	3.274416299	H12634		other
42283	3.2731086284	T94343	Homo sapiens M962 protein spliced isoform 2 mRNA complete cds	other
12809	3.271352097	AA424406	ESTs	other
36285	3.2696023617	AA424469	ESTs	other
21555	3.2666296446	R33073	EST	?
13767	3.2665695616	AA463234	ESTs	TM
4738	3.2661591937	U58766	Human FX protein mRNA complete cds	other
7258	3.263106866	AA075427	ESTs	other
17041	3.2629042076	AA070364	EST - RC_AA070364	?
15504	3.2616745245	W28362	ESTs	other
23793	3.2611829896	T90971	EST - RC_T90971	other
18214	3.2572346955	AA196635	ESTs	TM
7401	3.257164123	AA094800	Human translation initiation factor eIF3 p66 subunit mRNA complete cds	other
18912	3.2553600001	F10913	Homo sapiens clone 23617 unknown mRNA partial cds	other
36317	3.2509495347	AA425089	Human mRNA for KIAA03:34 gene complete cds	?
9410	3.2507279851	H20443	H.sapiens mRNA for TRE <sup>E</sup>	other
2146	3.2464307696	L41390	EST - L41390	?
18683	3.240814336	F04258	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]	?

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				?	?
33891	3.2392191408	AFFX-HUMTFRR/M11507_M			
14435	3.2372161315	/M11507 AA608730	ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA [Giardia intestinalis] ESTs Highly similar to GTP-BINDING PROTEIN LEPA	other	other
9584	3.2363829855	H88128	[Pseudomonas fluorescens]	TM	?
22061	3.2340098572	R49216	ESTs	?	?
35796	3.233287605	AA410223	EST - RC_AA410223	other	other
37403	3.2261852043	AA453613	ESTs	SS,	other
15796	3.2260359988	X16889	ALPHA-GALACTOSIDASE PRECURSOR	other	other
15840	3.2257932439	X70944	PTB-ASSOCIATED SPLICING FACTOR	other	other
7518	3.2252170427	AA147144	EST - AA147144	other	other
32335	3.2228388982	R78248	ESTs	other	other
3256	3.2180538038	M92439	130 KD LEUCINE-RICH PROTEIN	other	other
4400	3.2173898081	U41387	Human Gu protein mRNA partial cds	other	other
7681	3.2074414299	AA206983	Homo sapiens mRNA for DRIM protein	other	other
15676	3.2041299443	W68649	ESTs	TM	other
39590	3.2038953621	F09281	ESTs	?	?
26883	3.1980022253	AA291921	ESTs Weakly similar to putative p150 [H.sapiens]	other	other
9808	3.1920380384	M80627	Transcription factor 12 (HTF4 helix-loop-helix transcription factors 4)		
27755	3.1900699454	AA453444	ESTs	?	?
29983	3.1882280623	N26011	ESTs	other	other
21350	3.1876957756	R15846	ESTs	other	other
11981	3.1870525747	AA280928	ESTs		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			UNIGENE ID	DESCRIPTION	
23930	3.1817500097	T96690	ESTs	Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
30399	3.1792054412	N45226	EST		?
22286	3.1781990049	R59312	ESTs		other
13494	3.1673900969	AA453431	ESTs		TM
12908	3.1530533441	AA427579	ESTs		other
22319	3.1469419301	R60567	ESTs		TM
31309	3.1466750623	N66818	ESTs		TM
31192	3.1458779823	N64406	ESTs		other
11288	3.144853134	AA196512	ESTs		TM
170	3.1430726349	D00596		Thymidylate synthase	?
5307	3.1347905628	U90549		Human non-histone chromosomal protein (NHC) mRNA complete cds	other
26105	3.1311103325	AA243133		Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds	other
11659	3.1281786108	AA251909		Homo sapiens MAD3-like protein kinase mRNA complete cds	other
19177	3.124408565	H10984	ESTs		TM
8389	3.1241545824	AA425230	ESTs		TM
34087	3.1216555797	AA205125		Protein serine/threonine kinase stk2	other
25001	3.1209327466	AA004718	ESTs	ES is Weakly similar to B4/P31 protein [H.sapiens]	other
14149	3.1198500308	AA489665	ESTs		other
10167	3.1191986923	R55076	ESTs		other
17380	3.1071055868	AA102566	ESTs		other
42397	3.1044680628	W42928	ESTs		other
14935	3.1042015743	T94828	ESTs	Weakly similar to G $\alpha$ BINDING PROTEIN BETA-2 CHAIN [H.sapiens]	other
41673	3.1030349819	R78618	ESTs	Weakly similar to GTP-binding protein rab10 [R.norvegicus]	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
2750 3190	3.1026223619 3.1026223619	M35999 M86808	Integrin beta 3 (platelet glycoprotein IIIa antigen CD61) PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR	?	?
17406 598	3.0999394188 3.0912414004	AA112979 D59253	Homo sapiens mRNA for 'VRK1' complete cds Homo sapiens mRNA for low molecular mass ubiquinone-binding protein complete cds	other other	
29348 14130 14134	3.0802365759 3.0744457534 3.069660341	H69021 AA489041 AA489080	ESTs ESTs ESTs	other other other	
42421 15723	3.0684159011 3.0660746209	W45491 W79060	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]	other other	
11140	3.0650815198	AA1158132	ESTs Weakly similar to T23G11.7 [C.elegans] ESTs Highly similar to ribosome-binding protein p34 [R.norvegicus]	other other	
28531 2021	3.0649767987 3.0628707497	C20679 L34409	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae] Homo Sapiens (clone B3E13E13) chromosome 4p16.3 DNA fragment	?	
14522	3.058260163	AA610108	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schizosaccharomyces pombe]	SS,	
29853 15962 6541 13229 27315 13621	3.0545821815 3.0521475703 3.0509806038 3.0485366337 3.046622812 3.0302305369	N22162 Z21420 X95632 AA443811 AA424038 AA456821	ESTs ESTs Human Abl interactor 2 (Abl-2) mRNA complete cds ESTs ESTs ESTs	other other other other other other	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	mRNA
35929	3.0269182409	AA412429	Homo sapiens RRM RNA binding protein Gyr-rbp (GRY-RBP)	other	other
17925	3.0253428426	AA164209	mRNA complete cds	other	other
5053	3.0249536782	U76992	Human Tat-SF1 mRNA complete cds	other	?
15060	3.0213293848	U54999	Human LGN protein mRNA complete cds	other	?
17757	3.0205801351	AA147224	EST	other	other
19050	3.0192379314	H05509	ESTs	other	other
26530	3.0176823278	AA278650	Homo sapiens mRNA for KIAA0648 protein partial cds	TM	?
16806	3.0158779932	AA053258	Homo sapiens ribonuclease P protein subunit p40 (RPP40)	other	?
29088	3.0149440394	F13700	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds	TM	other
22960	3.0141662421	T10272	ESTs	other	other
33585	3.0121672451	W93000	ESTs	TM	?
220	3.0109180714	D13627	Human mRNA for KIAA0002 gene complete cds	TM	?
4298	3.0024671064	U36448	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM	?
7445	2.9995643641	AA104023	ESTs	?	?
40903	2.9990347068	N68670	ESTs	?	?
18055	2.997386648	AA179387	ESTs	other	other
7282	2.9962792596	AA083339	ESTs	other	TM
9348	2.9949017671	H03686	ESTs	?	?
806	2.9877476515	D87009	Human (lambda) DNA for immunoglobulin light chain	other	?
38447	2.9876031644	AA504255	Human protein kinase ATF1 mRNA complete cds	?	?
41464	2.9870604981	R46837	ESTs	other	?
9662	2.9869352306	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	EST	?
16976	2.9801154057	AA063625	EST	other	?
37426	2.9756408909	AA454016	ESTs	other	?

**FIG.-8BX**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				?	?
2588	2.9725898298	M27878	Zinc finger protein 84 (HIF2)	other	other
15174	2.9695024379	U82987	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds	other	other
33620	2.9657446567	W93943	ESTs	other	other
6784	2.965506112	Y11681	Homo sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds	?	?
41077	2.9642389716	N95028	ESTs	TM	?
1932	2.960985996	L24804	Human (p23) mRNA complete cds	other	other
39556	2.9588964022	F03738	ESTs	SS,	?
16108	2.9574232912	AA002258	ESTs	?	?
32156	2.9574232912	R40381	ESTs	other	other
13617	2.9552305838	AA456646	ESTs	other	other
11989	2.955203991	AA281251	ESTs	TM	?
6056	2.947654132	X68194	Parathyphsin [human keratinocyte line HaCaT mRNA 2106 nt]	other	?
15446	2.9445456286	W27374	Homo sapiens 10kD protein (BC10) mRNA complete cds	EST	?
38086	2.9445277634	AA482557	ESTs	other	other
13878	2.9444133384	AA476604	H.sapiens PAP mRNA	other	?
6209	2.9422425032	X76770	Phosphatidylinositol glycan class A (paroxysmal nocturnal hemoglobinuria)	EST - HG4755-HT5203	?
388	2.9357591919	D28791	EST - HG4755-HT5203	other	?
1351	2.9266145582	HG4755- HT5203	ESTS	other	?
42624	2.9266145582	W87804	ESTS	other	?
34895	2.9242794509	AA311972	ESTS	other	?
20157	2.9214162976	N23393	ESTS	other	?
29248	2.9188102156	H52918	ESTS	other	?
4893	2.9178533564	U66615	Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA complete cds	other	?

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**FIG.\_8By**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
10104	2.9150324884	R23855	ESTs	TM	?
15039	2.9147218324	U46116	Protein tyrosine phosphatase receptor type gamma polypeptide	?	?
1605	2.9141775797	L00058	V-myc avian myelocytomatisis viral oncogene homolog	?	?
4536	2.907560336	U48705	Receptor protein-tyrosine kinase EDDR1	?	?
10173	2.905710598	R56678	ESTs Weakly similar to cell division control protein CDC21 [H.sapiens]	?	?
26555	2.9056210172	AA279071	ESTs Weakly similar to T08A11.2 [C.elegans]	other	other
4401	2.9047655582	U41515	Human deleted in split hand/split foot 1 (DSS1) mRNA complete cds	other	other
21009	2.89950111918	N90401	ESTs	TM	?
3602	2.894817322	U01317	HEMOGLLOBIN EPSILON CHAIN	?	?
4833	2.8919254016	U63455	Sulfonylurea receptor (hyperinsulinemia)	?	?
36200	2.89112301426	AA421164	ESTs	?	?
26645	2.88998309441	AA281076	ESTs	other	other
35299	2.8887661574	AA3998622	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	other	other
9804	2.8880347344	M74558	Human SII mRNA complete cds	other	other
5216	2.8877977515	U83410	Human CUL-2 (cul-2) mRNA complete cds	other	other
12313	2.8847621603	AA397916	ESTs	?	?
5928	2.8836060438	X62048	WEE1-LIKE PROTEIN KINASE	TM	?
39586	2.8818258313	F09155	ESTs	?	?
34758	2.8775214637	AA287680	EST	other	other
18199	2.8753649024	AA195318	ESTs	?	?
19867	2.8720974689	H61476	ESTs	SS, TM	SS, TM
6081	2.8679372936	X69398	CD47 antigen (Rh-related antigen integrin-associated signal transducer)		

**FIG.-8BZ**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
5254	2.862087239	U86782	Human 26S proteasome-associated pad1 homolog (POH1)		other
13579	2.8570620494	AA455967	mRNA complete cds		?
1117	2.8568053461	HG3075-HT3236	Human neuronal PAS2 (NPAS2) mRNA complete cds		?
20533	2.8564678641	N54407	ESTs	TM	other
38495	2.8562453397	AA505118	Human nucleoporin 98 (NUP98) mRNA complete cds		?
33729	2.8548155651	Z39654	EST	EST	other
2028	2.8532776139	L35035	RIBOSE 5-PHOSPHATE ISOMERASE		other
27374	2.8520674335	AA425816	ESTs Weakly similar to Y53C12A.3 [C.elegans]		other
19404	2.8518690748	H20568	ESTs	other	other
26108	2.8504706329	AA243189	ESTs	SS,	SS,
4189	2.8439972255	U30930	UDP glycosyltransferase 3 (UDP-galactose ceramide galactosyltransferase)	TM	TM
16708	2.8427388072	AA043944	ESTs	other	other
357	2.8350474214	D26156	Human mRNA for transcriptional activator hSNF2b complete cds		other
26045	2.8315740098	AA236276	ESTs	ESTs	other
17796	2.8312342777	AA150435	ESTs	ESTs	other
8059	2.8288722809	AA310967	ESTs Weakly similar to T04A8.11 [C.elegans]		other
40914	2.827999584	N69220	ESTs	other	other
27169	2.8263163852	AA410287	H.sapiens mRNA for basic transcription factor 2 34 kD subunit		other
21358	2.8262413945	R16079	ESTs	other	other
3572	2.8261469131	S87759	Protein phosphatase 2C alpha [human teratocarcinoma mRNA 2346 nt]		other
11877	2.8259099942	AA262727	ESTs	other	?
1653	2.8234017508	L05424	CD44 antigen (cell adheses on molecule)		other
24645	2.8131264428	Z39106	ESTs		other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
35830	2.8126257031	AA411448	ESTs	TM	?
4433	2.8114422177	U43279	EST - U43279	?	other
20151	2.8109454503	N22895	Homo sapiens clone 1400 unknown protein mRNA partial cds	other	other
38648	2.8084431065	AA599267	EST - RC_AA599267	other	other
7777	2.8071817929	AA236820	ESTs	?	?
32845	2.80583194	W31566	EST	other	other
28258	2.8043934182	AA505133	ESTs	?	?
6853	2.798263202	Z22951	TRANSCRIPTION FACTOR P65	?	?
35944	2.7913872996	AA412488	ESTs	?	?
30648	2.7866523676	N50971	ESTs	?	?
18965	2.7857482775	H01411	ESTs	?	?
8616	2.785444221	AA460077	ESTs	?	?
14945	2.7838257917	T99606	ESTs Weakly similar to F35G2.2 [C.elegans]	?	?
8375	2.7805657722	AA422160	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds	?	?
34929	2.7792111121	AA342084	EST - RC_AA342084	?	?
326	2.7786978435	D21262	Human mRNA for KIAA0035 gene partial cds	?	?
27057	2.7781218063	AA400998	ESTs	?	?
36292	2.7746002184	AA424513	EST - RC_AA424513	?	?
6480	2.7735431318	X91788	H.sapiens mRNA for Icn1 protein	?	?
15424	2.7731675808	W27054	APOLIPOPROTEIN A1 REGULATORY PROTEIN-1	?	?
11602	2.7730818255	AA243007	ESTs	?	?
18175	2.77056686	AA194730	ESTs	?	?
25202	2.7698585996	AA034527	EST	?	?
1681	2.7697545972	L07493	Replication protein A (E coli RecA homolog RAD51 homolog)	?	?
14566	2.767984858	AA621122	ESTs	?	?
25614	2.7633374335	AA115769	ESTs	?	?

**FIG.-8Cb**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ESTs	ESTs
14182	2.7606048934	AA490885		other	other
31599	2.7591187958	N72196		other	other
18253	2.7471964081	AA206370		other	other
6193	2.7442487702	X76092	Regulatory factor (trans-acting) 3	other	other
22911	2.7433498559	T03865		other	other
35549	2.743246906	AA401274	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP)	mRNA complete cds	other
35955	2.7389431758	AA412528	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]	ESTs	other
17642	2.7377607284	AA132983	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H.sapiens]	ESTs	other
6131	2.7371784571	X72841	Human retinoblastoma-binding protein (RbAp46) mRNA	complete cds	other
41429	2.7347564467	R44994	ESTs	other	other
17052	2.7323944161	AA070815	EST - RC_AA070815	ESTs	?
34243	2.7294147034	AA235050	Homo sapiens TLS-associated protein TASR-2 mRNA	complete cds	other
22937	2.7284347248	T10065	Human tumor susceptibility protein (TSG101) mRNA	complete cds	other
5183	2.7243199196	U82130		ESTs	other
30837	2.7231409239	N54416		ESTs	other
16243	2.7228028265	AA012902		ESTs	TM
19954	2.7215193495	H80100		ESTs	other
6444	2.720441384	X89750	H.sapiens mRNA for TGF <sup>+</sup> protein		other
5916	2.7192579481	X61072	Human mRNA for T cell receptor clone IGRA17		SS,
6240	2.7168544194	X78627	H.sapiens mRNA for translin		?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				EST - RC_T69924	EST - RC_T69924
42116	2.7144176166	T69924		other	
7701	2.7107230468	AA215333		TM	
17568	2.7096978968	AA128905		TM	
42534	2.7086014274	W73189	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	SS, TM	
29813	2.708372123	N21111		other	
38898	2.7067394943	AA609458		other	
10316	2.7055636457	R88880	ESTs Moderately similar to zinc finger protein [M.musculus]	other	
14769	2.7040821985	S54641	HZF-16	other	
32961	2.7012196407	W38366	Human mRNA for KIAA0005 gene complete cds	other	
35273	2.6975345483	AA398507		other	
10180	2.6960696303	R60100		?	
32563	2.6955462902	T27697	Human mRNA for KIAA0036 gene complete cds	other	
34502	2.6948574449	AA262768		TM	
13223	2.6912995353	AA443720		other	
8494	2.6908515739	AA443460		other	
7776	2.6900717525	AA236771		other	
10400	2.6898958951	AA007234		other	
1130	2.6897527619	HG3132-HT3308		?	
2379	2.6874247447	M16937	Human homeo box c1 protein mRNA complete cds	TM	
18906	2.6861450774	F10868	Human SH3 domain-containing protein SH3P18 mRNA complete cds	?	
34796	2.6853510115	AA291259		TM	
41955	2.6821406177	T33311	Neuronal pentraxin II	other	
2009	2.6791061739	L33881	Protein kinase C iota	?	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	?
33688	2.6775081286	Z38501	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]	other	?
1385	2.6771402807	HG884-HT884	EST - HG884-HT884	other	?
24758	2.6756080868	Z40075	ESTs	other	?
7620	2.6742248913	AA192484	ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 [S.cerevisiae]	other	?
30733	2.6739544496	N52078	Homo sapiens mRNA for KIAA0637 protein complete cds	other	?
21256	2.6723253055	R09195	Homo sapiens mRNA for KIAA0564 protein partial cds	other	?
40528	2.669020458	N29325	ESTs Highly similar to 47 KD PROTEIN [Pseudomonas chlororaphis]	other	?
25285	2.6685455408	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	other	?
9296	2.667949532	D82775	ESTs Weakly similar to unknown [S.cerevisiae]	SS,	?
12174	2.6669305328	AA292128	ESTs	other	?
38357	2.6652770538	AA491265	EST	TM	?
3154	2.6619596806	M83712	Cholinergic receptor nicotinic alpha polypeptide 5	TM	?
7383	2.655440738	AA093834	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S.cerevisiae]	other	?
1923	2.6530372325	L23808	Matrix metalloproteinase 12 (macrophage elastase)	SS,	?
24906	2.6527048053	Z41840	ESTs	other	?
34726	2.6495430564	AA287278	ESTs	SS,	?
30407	2.6495430564	N45983	ESTs	TM	?
20408	2.6459891347	N48787	ESTs Moderately similar to !!! ALU SUBFAMILY SC	other	?
7158	2.6455059455	AA037206	WARNING ENTRY !!! [H.sapiens]	TM	?
26286	2.6445109706	AA253351	ESTs	?	?
19822	2.6431968212	H58684	ESTs	?	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE ID	DESCRIPTION	
12379	2.6428192941	AA399418		Homo sapiens mRNA for JM23 protein complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))	other
			R89287	ESTs	other
22698	2.6396306055		W58015	ESTs	other
24161	2.6394502284		H81497	ESTs	TM
9558	2.6370149706		AA188801	ESTs	other
18104	2.6358767288		Z41563	ESTs	other
24882	2.6357248889		H69485	ESTs	other
40038	2.6347974764		AB002359	Human mRNA for KIAA0361 gene KIAA0361 protein	other
8865	2.6344845492		R51831	ESTs	other
22148	2.6288326966		U51990	Human hPrp18 mRNA complete cds	other
4627	2.62777060831		AA426156	ESTs	TM
8394	2.6275394634		N49300	ESTs	other
20422	2.6272599716		R67258	ESTs Moderately similar to rhotekin [M.musculus]	other
41602	2.6258613824		D63480	Human mRNA for KIAA0146 gene partial cds	TM
612	2.6257836682		U62801	Human protease M mRNA\ complete cds	SS,TM
4821	2.619521444		AA053296	ESTs	other
16807	2.617722928		W07562	ESTs Moderately similar to rA8 [R.norvegicus]	other
15288	2.6173997018		AA481066	ESTs	other
38023	2.6135617291		T91715	ESTs Highly similar to HYPOTHEICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]	TM
23822	2.6120077647			ESTs RETINOBLASTOMA BINDING PROTEIN P48	
10951	2.6116018519		AA126719	other	
6150	2.6113980879		X74262	other	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
39336	2.6109987712	C20945	ESTs Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]		other
	17793	AA150242	ESTs Highly similar to modulator recognition factor 2 [H.sapiens]		other
	2.6085107387	AA292659	ESTs		other
	2.607468576	L42621	Homo sapiens Ly-9 mRNA complete cds		TM
	2.6048724507	AA040149	Human Chromosome 16 3'AC clone C1T987SK-A-270G1		other
	2.6031453592	U41816	Human C-1 mRNA complete cds		other
	2.6019047419	AA215299	Homo sapiens chromosome 19 cosmid R30783		other
	2.6011828937	X95654	Homo sapiens mRNA for SCP-1 complete cds		other
	2.5993684878	N62122	ESTs		other
	2.5993311375	AA207114	ESTs		other
	11308	U24704	Human antisecretory factor-1 mRNA complete cds		other
	4086	AA598938	EST - RC_AA598938		other
	2.5966362866	AA258189	ESTs		other
	2.5963996726	AA454103	ESTs		other
	2.5961501969	AA521186	ESTs		TM
	38615	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'		other
	11819	H59617	ESTs Highly similar to UENQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]		other
	37433	2.5957446266	ESTs		?
	2.5939657529	AA485147	ESTs Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]		other
	5587	2.5932338399	EST		?
	19841	2.5930132063	ESTs Weakly similar to Yel007c-ap [S.cerevisiae]		other
	10655	2.5925442731	EST		?
	14053	2.5899324577	AA4040882		
			AA485147		
	31574	2.5883094453	N71303		
	7614	2.5870699315	AA187579		
	37971	2.5847445397	AA479195		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE ID	DESCRIPTION	
7090	2.5845365105	AA009913	Homo sapiens diphthamide biosynthesis protein-2 (DPH2)	mRNA complete cds	other
17852	2.5841100415	AA156360	ESTs	ESTs	other
24219	2.5823376094	W69960	ESTs	Human clone 23960 mRNA sequence	other
19070	2.5813645258	H05970	EST	?	other
17719	2.5803606155	AA136569	EST	Human mRNA for KIAA0133 gene complete cds	TM
38669	2.579196791	AA599694	ESTs	Human mRNA for KIAA0133 gene complete cds	TM
20982	2.5763957078	N79565	ESTs	Homo sapiens breakpoint cluster region protein 1 (BCRG1)	other
9158	2.5731838907	D31446	mRNA complete cds	mRNA complete cds	other
11362	2.5731137778	AA227261	ESTs	Homo sapiens mRNA for KIAA0648 protein partial cds	TM
8613	2.5723119462	AA459555	ESTs	Homo sapiens mRNA for KIAA0648 protein partial cds	SS,
13866	2.5715997844	AA476319	ESTs	Ataxia telangiectasia mutated (includes complementation	?
10303	2.5712815907	R86178	groups A C and D)	groups A C and D)	?
22299	2.567916035	R59601	EST	EST - RC_AA206591	other
18257	2.5673459608	AA206591	ESTs	PUTATIVE 60S RIBOSOMAL PROTEIN	other
20555	2.5654242568	N55168	ESTs	Human chromosome 3p21.1 gene sequence complete cds	other
39552	2.5645918108	F03605	ESTs	Human mRNA for KIAA0C07 gene partial cds	other
27530	2.5631130948	AA435999	ESTs	Protein phosphatase 2 (formerly 2A) regulatory subunit B	other
1795	2.5608471476	L13434	ESTs	(PR 52) alpha isoform	other
14746	2.5603154966	D60354	ESTs	ES Ts Moderately similar to PTTG gene product [R.norvegicus]	?
2993	2.5587815672	M64929	ESTs	Human Cdc5-related protein (PCDC5RP) mRNA complete cds	other
19191	2.5545260975	H11297			
12986	2.5507999853	AA430032			
15452	2.5488533884	W27451			

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ORF	TM
18003	2.5465671712	AA171692	ESTs	other	
24198	2.5461854497	W67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM	
42653	2.5447526627	W92703	ESTs	other	
26446	2.544106171	AA258796	EST Weakly similar to putative p150 [H.sapiens]	?	
30438	2.5368548574	NA7204	ESTs Weakly similar to C50F4.12 [C.elegans]	other	
36365	2.5362912735	AA425893	ESTs Weakly similar to probable CBP3 protein homolog [C.elegans]	other	
26135	2.535658968	AA243765	ESTs	other	
41885	2.5349932888	T23449	ESTs Moderately similar to ZNF127-Xp [H.sapiens]	SS,	
15457	2.5343495968	W27560	ESTs	other	
27748	2.5320767519	AA453159	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	other	
32315	2.5302979959	R69840	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]	?	
25310	2.5274401579	AA046745	ESTs	other	
42720	2.5222453766	Z39436	ESTs	other	
12939	2.5200945911	AA428204	ESTs	other	
30746	2.5198420998	N52243	ESTs	other	
2222	2.5193624578	L76703	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds	?	
11609	2.5191765545	AA243303	ESTs	TM	
9658	2.5185814336	L16991	Deoxythymidylate kinase	other	
12210	2.5172044681	AA293774	ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL [C.elegans]	other	
3563	2.5169918533	S83364	EST - S83364	other	
42407	2.5128230047	W44768	Homo sapiens nephrocystin (NPHP1) mRNA partial cds	?	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENIE DESCRIPTOR		STRUCTURAL INFO
			UNIGENIE DESCRIPTOR	STRUCTURAL INFO	
32826	2.5128052161	W20291	Human mRNA for kinesin-related protein partial cds	other	
9692	2.5119977118	L37747	LAMIN B1	?	
27862	2.5094571267	AA458908	ESTs	TM	
33691	2.509287494	Z38630	EST	other	
17288	2.5088624644	AA085178	ESTs	SS, other	
9888	2.5076170902	N35449	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]	other	
5932	2.5073880985	X62153	Minichromosome maintenance deficient ( <i>S. cerevisiae</i> ) 3	other	
15885	2.5053862932	X95073	H.sapiens mRNA for translin associated protein X	other	
17952	2.5049193223	AA165677	ESTs Weakly similar to F16A11.1 [C.elegans]	other	
12197	2.5042458391	AA293206	ESTs	other	
6210	2.5042034458	X76942	Homo sapiens golgin-245 mRNA complete cds	other	
34047	2.5041917773	AA194166	ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]	other	
16929	2.5034461307	AA058952	ESTs	other	
26834	2.5028075682	AA287138	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]	other	
5157	2.50117270258	U80034	Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds	other	
38434	2.5005880672	AA497013	ESTs	?	
33269	2.5000262771	W72967	ESTs	other	
26991	2.4990009911	AA398284	ESTs	other	
7590	2.4948786183	AA173505	ESTs	other	
14960	2.4896232864	U05237	IN PHO2-POL3 INTERGENIC REGION [ <i>S.cerevisiae</i> ] Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds	other	

**FIG.-8Cj**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE: DESCRIPTOR			STRUCTURAL INFO
			ESTs	ESTs	ESTs	
13585	2.4866752902	AA455999	ESTs	ESTs	ESTs	other other other other other other other ?
35901	2.4847673158	AA412151	ESTs	ESTs	ESTs	other other other other other other other ?
38185	2.4826740426	AA487508	Homo sapiens mRNA for KIAA0688 protein complete cds			
34678	2.4824371274	AA284744	Annexin XI (56kD autoantigen)			
1424	2.4811113231	J02645	Eukaryotic translation initiation factor 2A			
16778	2.4800522256	AA047008	ESTs	EST - RC_R43286	ESTs	?
21876	2.4789005203	R43286	ESTs	ESTs	ESTs	other other other other ?
17779	2.4695725489	AA149641	ESTs	ESTs	ESTs	?
24559	2.4682754649	Z38588	ESTs	ESTs	ESTs	?
7781	2.467947166	AA242904	Homo sapiens proline-rich Gla protein 1 (PRGPP1) mRNA complete cds	ESTs	ESTs	?
7474	2.4677129013	AA126592	ESTs	ESTs	ESTs	other other other ?
34290	2.4675279697	AA236866	Human clone 23574 mRNA sequence			TM
5316	2.4673813483	U90905	ESTs	ESTs	ESTs	other
10218	2.4645666539	R68884	ESTs	ESTs	ESTs	?
18109	2.4634292267	AA188981	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds	ESTs	ESTs	?
6485	2.4613518897	X92098	H.sapiens mRNA for transmembrane protein rmp24			SS, TM ?
34954	2.4591845976	AA342959	EST - RC_AA342959			?
42558	2.4588830205	W74751	ESTs	ESTs	ESTs	other other other ?
27444	2.4585750563	AA430160	ESTs	ESTs	ESTs	other other other ?
21284	2.45822503599	R10301	Homo sapiens cancer associated surface antigen (RCAS1)			?
8920	2.4568596729	AF006265	mRNA complete cds			other
30037	2.4544484116	N27439	ESTs	ESTs	ESTs	TM

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ESTs	TM
27602	2.4527990177	AA443702	ESTs Weakly similar to WC2B12.7 [C.elegans]	ESTs	TM
3390	2.4525517032	SS9184	RYK receptor-like tyrosine kinase	ESTs	TM
25040	2.452352841	AA010188		ESTs	other
37713	2.4487800271	AA461317		ESTs	other
40477	2.4477660739	N24006	Homo sapiens BAC clone RG300E22 from 7q21-q31.1	ESTs	other
29382	2.4470532391	H72914		ESTs	other
35521	2.4465885249	AA400831		ESTs	other
20324	2.4464518504	N35406	Phospholipase C beta 4	ESTs	SS, ?
18620	2.4460334893	F02506		ESTs	other
21087	2.4406971835	R00186		EST	other
9950	2.4398530157	N71503		ESTs	SS,
31965	2.4363228422	N93629		ESTs	TM
15120	2.4345895403	U73524	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds	ESTs	
28813	2.4339770686	D59257	Human C-1 mRNA complete cds	ESTs	
38082	2.4295434916	AA482284		ESTs	
34723	2.428289395	AA287115		ESTs	
7960	2.427332589	AA285277	Homo sapiens brain expressed ring finger protein mRNA complete cds	ESTs	
18073	2.4231729031	AA180453		EST	other
36755	2.4222443392	AA435698		EST - RC_AA435698	other
18927	2.4187841215	F11087		ESTs	other
3457	2.4186224787	S74728	Antiquitin	ESTs	TM
38606	2.4177693475	AA598844		ESTs	other
20967	2.41519947	N76086		ESTs	other
24752	2.4141498374	Z40012	Homo sapiens mRNA for KIAA0587 protein complete cds	ESTs	other
28443	2.4138974256	AA621611		ESTs	?

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
452	2.4135942278	D38076	RAN binding protein 1		other
11701	2.4134095351	AA253031	Homo sapiens RRM RNA binding protein GRY-RBP		other
13655	2.412509306	AA458919	mRNA complete cds		other
24822	2.4119066031	Z40956	ESTs Weakly similar to 263 proteasome subunit p44.5 [H.sapiens]		other
12672	2.41112720798	AA417067	ESTs		other
4836	2.4106618618	U63717	Human osteoclast stimulating factor mRNA complete cds		other
42200	2.4083828799	T83729	EST - RC_T83729		?
10987	2.4076548868	AA132239	ESTs Highly similar to HYPOTHETICAL 47.4 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]		other
35672	2.4073821434	AA404995	EST - RC_AA404995		other
6224	2.406310553	X77748	Glutamate receptor metabotropic 3		TM
28395	2.404213441	AA610064	ESTs		other
36390	2.4032664297	AA426291	ESTs Weakly similar to No definition line found [C.elegans]		other
21045	2.4031905697	N93403	ESTs		?
4558	2.4024665999	U49379	Human diacylglycerol kinase epsilon DGK mRNA complete cds		TM
12916	2.3998505067	AA427745	ESTs		other
20850	2.3998090334	N69514	ESTs Weakly similar to oxidoreductase [H.sapiens]		other
29759	2.3986103066	H99972	ESTs		other
36786	2.3971559161	AA435815	Human Clk-associated R5 cyclophilin CARS-Cyp mRNA complete cds		other
31942	2.3947415736	N93185	ESTs		other
7097	2.39382714	AA011452	ESTs		other
39462	2.3936147708	D60063	ESTs		other
14420	2.3919915706	AA600322	ESTs Highly similar to AAC-RICH mRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]		other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				+	
34629	2.3916035475	AA282527	EST - RC_AA282527	other	
27431	2.3905463084	AA429038	ESTs	TM	
6387	2.3904071666	X85372	H.sapiens mRNA for Sm protein F	other	
11342	2.3902176276	AA223874	Homo sapiens mRNA for KIAA0704 protein partial cds	other	
1497	2.388369765	J04088	Topoisomerase (DNA) II alpha (170kD)	other	
9841	2.38841922016	M95724	Centromere autoantigen C	other	
11454	2.3820201875	AA233854	ESTs	TM	
29950	2.3807499489	N24902	Homo sapiens mRNA for E1B-55kDa-associated protein	TM	
8396	2.3807187289	AA426176	ESTs Weakly similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]	other	
32978	2.38059995259	W42788	Human terminal transferase mRNA complete cds	other	
27872	2.3784145648	AA459254	ESTs	other	
11623	2.3769685069	AA243617	ESTs	other	
26582	2.3766957777	AA279768	ESTs	other	
22142	2.3761275381	R51382	Homo sapiens mRNA for KIAA0659 protein partial cds	other	
13533	2.3759359586	AA454607	ESTs Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]	other	
11534	2.3747649776	AA236223	ESTs	other	
5976	2.3709397882	X64229	DEK PROTEIN	other	
6231	2.3680994679	X78121	Choroideremia	TM	
2382	2.3677644584	M16967	Coagulation factor V	other	
22887	2.3673034941	T03314	ESTs	TM	
24371	2.3663729415	W87415	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other	
25286	2.3658134948	AA045261	ESTs	other	
9054	2.3647542793	C02472	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]	other	

**FIG.-8Cn**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE ID	DESCRIPTION	
8163	2.3646144577	AA357394	ESTs	Weakly similar to LINE/Ig H-chain fusion protein	other
12233	2.364077771	AA343513	ESTs	[M.musculus]	SS,
22924	2.3634007127	T08195	ESTs	Moderately similar to ALR [H.sapiens]	other
14371	2.361524453	AA599219	ESTs	Moderately similar to ALR [H.sapiens]	other
12401	2.3607293644	AA400229	ESTs	?	other
26169	2.3599633182	AA251089	ESTs	Weakly similar to ORF YOR281c [S.cerevisiae]	other
23065	2.3592943521	T23539	ESTs	Highly similar to zin: finger protein [M.musculus]	other
20524	2.358218239	N53965	ESTs	?	other
20837	2.3577032218	N69263	ESTs	Highly similar to HEXOKINASE TYPE I [Homo sapiens]	other
18201	2.3573132815	AA195398	ESTs	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1 the ADORA2B P adenosine A2b receptor LIKE pseudogene the IRF6	other
7813	2.3566868562	AA248297	ESTs	?	TM
21195	2.3547018746	R07210	ESTs	?	other
13377	2.3513919997	AA449720	ESTs	Homo sapiens clone 247(16 mRNA sequence	other
9714	2.3497245732	L44367	ESTs	?	other
41537	2.3460892052	R55673	ESTs	?	other
17352	2.34595172	AA100925	ESTs	?	other
11914	2.3446613991	AA278907	ESTs	?	other
24890	2.3440589932	Z41634	ESTs	?	other
28796	2.3434458024	D51272	EST - RC_D51272_S	?	other
36798	2.342525534	AA435870	ESTs	Weakly similar to B0564.1 [C.elegans]	other
22491	2.3409294581	R70012	EST	?	other
4798	2.3403776443	U61538	EST	Human calcium-binding protein chp mRNA complete cds	other
40847	2.3397210986	N66354	ESTs	?	other

**FIG.\_8Co**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
15657	2.3392349306	W63627	Small inducible cytokine A5 (RANTES)		TM
24482	2.3374046148	Z38137	ESTs		other
42022	2.3336939603	T53138	Homo sapiens mRNA for hTCF-4		TM
38233	2.3314220199	AA489023	ESTs		other
41221	2.3310635524	R21531	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]		other
8053	2.3297250374	AA309880	ESTs		?
363	2.3275393529	D26528	Human mRNA for RNA helicase complete cds		other
26679	2.3241677574	AA281733	ESTs		TM
13407	2.3216524472	AA450200	ESTs		TM
17955	2.3180957399	AA166703	ESTs		?
31858	2.3160841803	N90680	EST		SS,
24092	2.3151511584	W42845	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds		
16759	2.3118245547	AA046294	ESTs		other
7861	2.311355404	AA252436	Homo sapiens clone 2337c7 and 23917 mRNA partial cds		other
41176	2.3111568749	R09379	Natural resistance-associated macrophage protein 2		TM
3860	2.3104335895	U13913	Homolog of Drosophila skwpoke (potassium channel - calcium-activated)		TM
40886	2.3077403929	N68149	ESTs Weakly similar to ERV-INDUCED G PROTEIN- COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]		other
19428	2.3068982601	H22949	EST		?
36080	2.3048383557	AA417282	EST - RC_AA417282		other
27264	2.3043527378	AA418389	ESTs		other
13600	2.3031968696	AA456286	ESTs		other
13552	2.3026988375	AA454943	ESTs		other
15664	2.3025773291	W67456	ESTs Moderately similar to YY1-associated factor 2 [H.sapiens]		other

**FIG.\_8Cp**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	STRUCTURAL INFO	
26583	2.3025403178	AA279774	ESTs	?	?
37434	2.3013886299	AA454149	EST	other	other
7833	2.2992574443	AA249300	ESTs	other	other
3674	2.2985613315	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds	other	other
33694	2.2984566375	Z38770	ESTs	?	?
11178	2.2972286082	AA167436	ESTs	other	other
16977	2.2912855364	AA064616	ESTs	?	?
19799	2.290119924	H57330	EST	?	?
5948	2.2900738182	X63337	EST - X633337	?	?
42097	2.2881548729	T66318	Isoleucine-tRNA synthetase	other	other
24247	2.2881065691	W73010	Ribosomal protein L37	other	other
40879	2.2870463837	N67816	ESTs Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]	other	other
5875	2.2860441014	X59405	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)	?	?
22325	2.2850330577	R60777	ESTs	other	other
9621	2.2844572929	J05032	ASPARTYL-TRNA SYNTHETASE	other	other
9239	2.2823045248	D79100	ESTs	other	other
41997	2.2818672356	T47788	ESTs	?	other
31105	2.28091752	N63207	Replication factor C 37-kD subunit	other	other
39565	2.2794194837	F04320	Homo sapiens voltage dependent anion channel protein	other	other
7404	2.2793872556	AA094989	mRNA complete cds	other	other
6388	2.2788670475	X85373	H.sapiens mRNA for Sm protein G	other	other
20263	2.2729348551	N31952	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III [Caenorhabditis elegans]	other	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
			STRUCTURAL INFO	ORF
14529	2.2722894932	AA620307	ESTs	other
21197	2.2718368964	R07320	ESTs	other
28203	2.2692501412	AA490969	ESTs	other
38320	2.2687130032	AA490611	ESTs	other
41625	2.2680307053	R69333	ESTs	other
4674	2.265734645	U54999	Human LGN protein mRNA complete cds	other
28861	2.2637023919	D80037	EST Weakly similar to C50B8.3 [C.elegans]	other
31062	2.2633840539	N62827	ESTs	other
26756	2.2627797292	AA283832	ESTs	other
11567	2.2614480815	AA236747	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds	other
25050	2.2605083659	AA011134	ESTs Weakly similar to renin [H.sapiens]	?
41935	2.2593192037	T29681	Human serine kinase mRNA complete cds	TM
26895	2.2582367069	AA292765	H.sapiens mRNA for M-phase phosphoprotein mpp5	other
40585	2.2581993468	N34891	Homo sapiens mRNA for KIAA0595 protein partial cds	other
3343	2.2568482074	M97936	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	other
42435	2.2532463427	W46994	ESTs	other
5937	2.2489783488	X62534	High-mobility group (nonhistone chromosomal) protein 2	TM
21241	2.2477801609	R08617	ESTs	TM
25756	2.2472586561	AA135868	ESTs	other
34184	2.2459308213	AA227959	Human cysteine protease Mcch2 isoform alpha (Mcch2) mRNA complete cds	other
8672	2.2450864129	AA477046	ESTs	other
7387	2.2447544716	AA093977	ESTs	other
28822	2.2424116577	D59352	ESTs	TM
18016	2.2410305445	AA173223	ESTs	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	mRNA
20843	2.239288723	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds	ESTs	other
10054	2.2387950133	R10266	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2: INTERGENIC REGION [Saccharomyces cerevisiae]	ESTs	other
34094	2.2384154308	AA206088	ESTs	ESTs	other
41246	2.2380827238	R27296	ESTs	ESTs	other
22634	2.2346537819	R82837	ESTs	ESTs	other
19686	2.2319351858	H48502	ESTs	ESTs	SS,
34568	2.2306030547	AA280609	ESTs Weakly similar to KC2B2.3 gene product [C.elegans]	ESTs	other
28448	2.2295708871	AA621752	Human 26S proteasome- $\epsilon$ -associated pad1 homolog (POH1) mRNA complete cds	ESTs	other
20909	2.2284835116	N71704	ESTs	ESTs	SS,TM
651	2.2260753259	D78129	EST - D78129	ESTs	other
40409	2.2244318492	H99877	Homo sapiens exportin t mRNA complete cds	ESTs	other
20340	2.2244062527	N38825	ESTs	ESTs	other
20002	2.2233023294	H93005	EST - RC_H93005	ESTs	other
37321	2.2209252793	AA451898	ESTs	ESTs	other
8274	2.2208752623	AA402095	ESTs	ESTs	other
20221	2.219714612	N29345	ESTs	ESTs	other
5792	2.2186801223	X54941	CDC28 protein kinase 1	ESTs	other
4034	2.21808435	U21858	Human transcription initiation factor TFIID subunit TAFII31 mRNA complete cds	ESTs	other
36222	2.2149577598	AA421481	ESTs	ESTs	other
16567	2.2146935655	AA031591	Human mRNA for KIAA0139 gene complete cds	ESTs	other
4721	2.2134595068	U58046	Human Gu protein mRNA partial cds	ESTs	other
28656	2.2125017907	D19708	Human mRNA partial cds	ESTs	TM

**FIG.\_8Cs**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR	STRUCTURAL INFO	
				ORF	
20723	2.2113936194	N66093	H.sapiens mRNA for Nup88 protein	other	?
6714	2.2062571749	Y08612		ESTs	other
19240	2.2055839996	H13265		ESTs	other
36447	2.2050784323	AA428188		ESTs	other
11688	2.202413216	AA252672	Homo sapiens diphthamide biosynthesis protein-2 (DPH2)	mRNA complete cds	other
21650	2.2018153311	R37938	Homo sapiens KIAA0440 mRNA partial cds	ESTs	?
14152	2.2015953698	AA489790	Homo sapiens Ran-GTP binding protein mRNA partial cds	ESTs	?
42657	2.1975280207	W92771	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR	ESTs	?
4642	2.1968027789	U52427	Human RNA polymerase II subunit hsRNPB7 mRNA complete cds	ESTs	TM
32779	2.1962611079	W02102		ESTs	other
38341	2.1951559134	AA490967		ESTs	other
11803	2.1921143838	AA257971		ESTs	TM
34835	2.190705129	AA292677		ESTs	other
39085	2.1895804523	AA620599	MYB PROTO-ONCOGENE PROTEIN	ESTs	?
4046	2.1877764122	U22376	ESTs Weakly similar to house-keeping protein [M.musculus]	ESTs	other
11600	2.1876723705	AA242868	Human BRCA1-associated RING domain protein (BARD1)	ESTs	other
5051	2.1866660566	U76638	mRNA complete cds	ESTs	?
33917	2.1864855739	AA167323		ESTs	TM
20674	2.1858972155	N63392		ESTs	TM
41031	2.1768902734	N91246		ESTs	?
25114	2.1759894688	AA020923		EST	?
24711	2.1758363153	Z39645		ESTs	other
4733	2.1721786534	U58658	Human unknown protein mRNA within the p53 intron 1	ESTs	other
4871	2.1712198791	U66033	complete cds	ESTs	other
			Human glypican-5 (GPC5) mRNA complete cds	ESTs	

**FIG.-8Ct**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			FOLD	UPREGULATED	
29733	2.1687028853	H99398	EST	?	?
23155	2.1678113438	T30550	ESTs	other	?
34638	2.164515923	AA282987	EST	other	?
35541	2.1621480372	AA400986	Prothymosin alpha	?	?
1889	2.1598384252	L20591	Annexin III (lipocortin III)	?	?
15106	2.1591553963	U68111	PROTEIN PHOSPHATASE INHIBITOR 2	?	?
40131	2.1583553082	H79779	Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds	other	?
19516	2.158045763	H29207	EST	other	?
4136	2.1577799237	U28014	ICH-2 PROTEASE PRECURSOR	other	?
20276	2.1548737104	N32919	ESTs	other	?
13292	2.1546709291	AA447621	ESTs Highly similar to 40 KD PROTEIN [Bornavirus]	other	?
20666	2.154262609	N63165	ESTs	other	?
6065	2.1526648242	X68560	Sp3 transcription factor	other	?
18238	2.1516362853	AA205389	ESTs	other	?
21627	2.1515999154	R37410	EST	?	?
3438	2.1502571642	S72024	Eukaryotic translation initiation factor 5A	other	?
34648	2.1498935434	AA283772	ACTIVATOR 1 36 KD SUBUNIT	SS,	?
5964	2.1488964343	X63657	Follicular lymphoma variant translocation 1	other	?
13250	2.1466085975	AA446459	ESTs	other	?
34370	2.1465845856	AA251829	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPR7 INTERGENIC REGION [Saccharomyces cerevisiae]	ESTs	?
27996	2.145312871	AA470156	ESTs Weakly similar to dynein 74K chain cytosolic [R. norvegicus]	SS,	?
4408	2.1398865247	U41745	Human PDGF associated protein mRNA complete cds	other	?
4187	2.1395632136	U30888	Human tRNA-guanine transglycosylase mRNA complete cds	other	?
10804	2.1366859886	AA069549	ESTs	other	?

**FIG.-8Cu**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE	DESCRIPTOR	
34552	2.1340290702	AA279985	Human mRNA for KIAA0372 gene complete cds		other
18380	2.1331897016	AA227119	ESTs	other	other
5223	2.1298428563	U83843	EST - U83843	other	other
37415	2.1270169134	AA453807	EST	other	other
14582	2.1260941468	AA621340	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]	other	?
27756	2.123647107	AA453447	ESTs	other	other
13787	2.1232866197	AA463745	ESTs Highly similar to PRI-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	other	other
5173	2.1232706565	U81554	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	other	other
40029	2.11214337319	H68221	Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA complete cds	other	other
19972	2.1193721042	H83639	ESTs	other	other
23301	2.117519655	T52847	ESTs	other	other
20504	2.1134521605	N52966	ESTs	other	other
40145	2.1132200572	H81391	Human mRNA for histamine N-methyltransferase complete cds	SS,	other
3461	2.1131164397	S75256	EST - S75256	other	other
41893	2.1124189285	T23611	EST - RC_C14805	other	other
39298	2.1092181318	C14805	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens]	other	other
36021	2.1084566145	AA416876	ESTs Weakly similar to C5)B8.3 [C.elegans]	?	?
8382	2.1077406838	AA424199	ESTs Weakly similar to C5)B8.3 [C.elegans]	other	other
28288	2.1075593303	AA598447	Homo sapiens exportin t mRNA complete cds	other	other
5807	2.1071009331	X55740	5' nucleotidase (CD73)	other	?
19747	2.106109699	H53572	ESTs	other	other

**FIG.-8Cv**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
38155 924	2.1052335506 2.1037724222	AA486777 HG1112- HT1112	ESTs EST - HG1112-HT1112		TM ?
9544 8384 25165 24348 41401 35340 10898	2.1022261514 2.1005713227 2.1005132894 2.1000366838 2.0994968367 2.0993762592 2.0990741816	H72630 AA424282 AA027837 W86469 R43334 AA398900 AA112063	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds Retinitis pigmentosa 3 (X-linked recessive) Tropomyosin alpha chain (skeletal muscle) Homo sapiens KIAA0410 mRNA complete cds EST - RC_AA398900 ESTs Weakly similar to PRI-MRNA SPLICING HELICASE BRR2 [S.cerevisiae] Isoleucine-tRNA synthetase ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING	ESTs ESTs ESTs ESTs ESTs ESTs ESTs	other other SS, TM ? other other other
381 22051	2.0974305874 2.0971755	D28473 R49047	ENTRY !!! [H.sapiens] Testis specific protein Y-linked	ESTs ESTs	TM ?
3293 11528 11890 13643 19927 36511 2130	2.0965631118 2.0954548212 2.0952685865 2.0952581265 2.0952547855 2.0927695929 2.0925292202	M94893 AA236018 AA278323 AA458578 H71829 AA429632 L40407	ESTs Weakly similar to unknown [S.cerevisiae] Homo sapiens clone 24606; mRNA sequence Homo sapiens clone 24477; mRNA sequence ESTs ESTs Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds	ESTs ESTs ESTs ESTs ESTs ESTs ESTs	TM ? other other ?
7193 5448 35956 7525	2.0924678877 2.0921643167 2.0875765163 2.0870133892	AA046768 X02751 AA412533 AA149259	Homo sapiens clone TUA8 Cri-du-chat region mRNA Neuroblastoma RAS viral ( <i>v-ras</i> ) oncogene homolog	ESTs ESTs ESTs ESTs	other other other other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO		
				TM	other	other
39592	2.0862891765	F09351	ESTs Weakly similar to weakly similar to <i>S. cerevisiae</i> PTM11 precursor [C.elegans]	ESTs	other	other
28029	2.0855738844	AA478479		ESTs	other	other
18425	2.0855157851	AA232103		ESTs	other	other
23494	2.0843308862	T70045	ESTs Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN F26A3.7 IN CHROMOSOME I [C.elegans]	EST	?	other
30882	2.0840312831	N56906	Human TFIID subunit TAF155 (TAFI155) mRNA complete cds	EST	other	other
32597	2.0839196473	T47333		ESTs	other	other
33368	2.0838178514	W80814		ESTs	other	other
10259	2.0829121213	R77527		ESTs	other	other
21882	2.0825457608	R43365		ESTs	other	other
20590	2.0820571859	N58146		ESTs	other	other
12907	2.0807802388	AA427577		ESTs	other	other
22958	2.0770089467	T10264		ESTs	other	other
42044	2.0762746251	T58753		ESTs	other	other
4210	2.0750374179	U31814	Human transcriptional regulator homolog RPD3 mRNA complete cds	ESTs	other	other
39	2.074214716	AB003698	Homo sapiens mRNA for Cdc7-related kinase complete cds	ESTs	TM	other
14350	2.0739236064	AA598831		ESTs	other	other
29840	2.0729224128	N21680		ESTs	other	other
25593	2.0715918096	AA113149	Homo sapiens IPL (IPL) mRNA complete cds	ESTs	other	other
26071	2.0708411247	AA236880	Protein phosphatase 2A regulatory subunit B' alpha-1	EST	?	other
26529	2.0699045563	AA278594		ESTs	other	?
12154	2.0692192056	AA291293		ESTs	other	other
18817	2.0684614007	F10077		ESTs	other	other
6635	2.0674931973	X99585	H.sapiens mRNA for SMT3B protein	ESTs	other	other
6681	2.066065203	Y00971	Phosphoribosyl pyrophosphate synthetase 2	ESTs	other	other

**FIG.-8Cx**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			UNIGENE DESCRIPTOR	STRUCTURAL INFO	
22077	2.0647745388	R49482	ESTs	other	
11752	2.0645929355	AA256042	ESTs	other	
41257	2.0634413934	R31680	ESTs	SS, TM	
6904	2.0622381932	Z34897	Histamine receptor H1	other	
16879	2.060262971	AA056538	ESTs	other	
38040	2.0595449295	AA481403	ESTs	other	
4111	2.0567536207	U26312	Human heterochromatin protein HP1Hs-gamma mRNA complete cds	other	
32878	2.0546812272	W37448	ESTs	TM	
21743	2.0543668448	R40576	ESTs Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]	?	
25968	2.0525018401	AA234935	ESTs	other	
24659	2.0506511898	Z39211	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA complete cds	other	
38030	2.0505994824	AA481148	ESTs	other	
61	2.0484705331	AC002115	Cytochrome c oxidase subunit VIb	?	
6306	2.0474040935	X81625	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1	?	
8203	2.0473464771	AA382517	EST - AA382517	other	
34357	2.0469305727	AA251430	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 [Canis familiaris]	other	
36972	2.0468599712	AA442767	Tyrosine 3-monoxygenase/tryptophan 5-monooxygenase activation protein beta polypeptide	other	
28156	2.0459278063	AA489057	H.sapiens mRNA for nuclear protein SA-2	?	
24434	2.0456952222	W92787	ESTs	other	
33508	2.0449481783	W88772	Human DNA sequence from cosmid F0811 on chromosome 6. Contains Daxx BING1 Tapasin RGL2 KE2 BING4 BING5 ESTs and CpG islands	other	

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				EST	EST
37681	2.0449346104	AA460675	H.sapiens mRNA for TRE5	other	other
27125	2.0448698236	AA405505	Homo sapiens mRNA for putative RNA helicase 3' end	other	other
3780	2.0445300752	U09851	Zinc finger protein 148 (pHZ-52)	other	other
9112	2.0443252757	D16611	Coproporphyrinogen oxidase (coproporphyrin hydroxylase)	TM	TM
8357	2.044244223	AA418921	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	other	other
9133	2.0436113204	D30946	ESTs Highly similar to TRANSLOCON-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus]	TM	TM
7519	2.0414123824	AA147425	EST - AA147425_s	other	other
14701	2.0413755305	D59324	EST - D28423	?	?
380	2.0411495076	D28423	ESTS	other	other
30571	2.0348528804	N49595	Holocarboxylase synthetase (biotin-[propionyl]-Coenzyme A-carboxylase (ATP-hydrolysing) ligase)	TM	TM
825	2.0329522889	D87328	ESTs Weakly similar to HYPOTHETICAL PROTEIN HI0034 [Haemophilus influenzae]	other	other
27744	2.0318041265	AA4522818	Arginine vasopressin receptor 1 (AVPR1)	?	?
3997	2.0311208335	U19906	EST - RC_R91394	other	other
22717	2.0302732387	R91394	EST - D28364	other	other
377	2.0289078264	D28364	EST	other	other
28581	2.0274006652	C21163	ESTs Highly similar to PO122 PROTEIN [Saccharomyces cerevisiae]	other	other
11790	2.0269672127	AA256678	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other	other
37931	2.0269058272	AA478523	ESTs Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]	other	other
24678	2.0209818539	Z39349			

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**FIG.\_8C2**

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			FOLD	UNIGENE	
10940	2.0209035614	AA122217	ESTs	Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.elegans]	other
13964	2.0207518872	AA479048	ESTs	Homo sapiens clone 24538 mRNA sequence	?
15665	2.0197735666	W67631	ESTs		TM
28379	2.0189373185	AA609710	ESTs		other
13349	2.0172119305	AA449269	ESTs	Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]	SS,
7322	2.0167797945	AA090692	ESTs	Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]	other
29358	2.0165296752	H70641	ESTs	EST - RC_H70641	?
24230	2.016017562	W72276	ESTs		other
40212	2.0158778189	H88535	ESTs	Human clone 121711 defective mariner transposon Hsmar2	?
729	2.01573779	D83778	ESTs	Human mRNA for KIAA0194I gene partial cds	other
17951	2.0144787235	AA165526	ESTs	Homo sapiens bifunctional ATP sulfurylase/adenosine 5'-phosphosulfate kinase mRNA complete cds	other
33943	2.0135799277	AA171739	ESTs	Zinc finger protein 43 (HTFF1)	other
5870	2.0118426199	X59244	ESTs		other
36319	2.0116529739	AA425107	ESTs		other
25654	2.0097423819	AA126951	ESTs	ESTs Weakly similar to DNase-directed RNA polymerase [D.melanogaster]	other
16344	2.0090457727	AA018907	ESTs		?
8118	2.0090099575	AA328993	ESTs		other
29962	2.0087628098	N25228	ESTs		TM
32236	2.0078250756	R49327	ESTs	Natural resistance-associated macrophage protein 2	TM
3279	2.0072427596	M94065	ESTs	DIHYDROORotate DEHYDROGENASE PRECURSOR	TM
16255	2.0065069683	AA013349	ESTs		other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR			
			UNIGENE	INFO	STRUCTURAL INFO	ORF
37972	2.0059209236	AA479215	EST - RC_AA479215	TM	other	
41256	2.005858844	R31577	ESTs	other	other	
34834	2.0050133743	AA292655	ESTs	other	other	
23169	2.0039279023	T33215	ESTs	other	other	
29851	2.0034762995	N22145	ESTs	other	other	
32862	2	W32519	EST	?		

*FIG.\_8Db*

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NEW KEY NUMBER	ACCESSION NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE DESCRIPTOR
104660 130016	AA007160 AA055811	23 14	ESTs transmembrane glycoprotein SS SS, TM
104954	AA074514	10	ESTs; Moderately similar to (defline not available 4753768) [H.sapiens] ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans] Other
105082	AA143763	7	ESTs retinoic acid induced 3 ESTs; Weakly similar to PLICKSTRIN [H.sapiens] Human endogenous retroviral protease mRNA; complete cds ESTs ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens] H.sapiens HUNK1 mRNA ESTs ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens]
109141 108893 108927 109027 133015 114546	AA176428 AA135894 AA143493 AA157818 AA047036 AA056263	7 6 5 5 4 4	ESTs ESTs; Weakly similar to C17H11.6 [C.elegans] ESTs; Weakly similar to transformation-related protein [H.sapiens] ESTs ESTs ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens] Homo sapiens serine protease mRNA; complete cds ESTs; Weakly similar to C17H11.6 [C.elegans] ESTs; Weakly similar to transformation-related protein [H.sapiens] ESTs ESTs ESTs; Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro) Other Other SS Other
104974 108695 105049	AA085918 AA121315 AA132554	4 4 4	ESTs ESTs ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens] Homo sapiens serine protease mRNA; complete cds ESTs; Weakly similar to C17H11.6 [C.elegans] ESTs; Weakly similar to transformation-related protein [H.sapiens] ESTs ESTs ESTs; Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)
133834 109244 128411	AA147510 AA194237 AA007555	4 4 3	ESTs ESTs ESTs; Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)
114509 104888 114542 132718	AA043551 AA053660 AA055768 AA056731	3 3 3 3	ESTs ESTs ESTs ESTs; Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)

FIG.\_9Aa

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NEW KEY NUMBER	ACCESSION	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE DESCRIPTOR
104953	AA074157	3	ESTs GDP dissociation inhibitor 2; transmembrane 4 superfamily member 6
132784	AA099589	3	Other Other SS, TM SS
130962	AA102051	3	Other Other TM
134421	AA122386	3	Other Other ESTs
105035	AA128486	3	Other Other ESTs
105039	AA130349	3	Human mRNA for KIAA0069 gene; partial cds ESTs; Highly similar to CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN [H.sapiens]
105062	AA134968	3	Other Other ESTs
133617	AA148318	3	Other Other ESTs
130335	AA156499	3	Other Other ESTs
105132	AA159501	3	Other Other ESTs
109042	AA159525	3	Other Other ESTs
109043	AA159605	3	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens]
132669	AA188378	3	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens] nuclear receptor coactivator 4
135398	AA194075	3	ESTs ESTs; Highly similar to rap2 gene product [H.sapiens] ESTs; Weakly similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]
109344	AA213696	3	ESTs ESTs; Weakly similar to sirilar to WW/rsp5/WWP domain containing proteins [C.elegans]
133221	AA235289	3	ESTs ESTs; Weakly similar to sirilar to WW/rsp5/WWP domain containing proteins [C.elegans]
114496	AA035611	2	ESTs ESTs; Weakly similar to sirilar to WW/rsp5/WWP domain containing proteins [C.elegans]
128635	AA043959	2	ESTs ESTs; Weakly similar to sirilar to WW/rsp5/WWP domain containing proteins [C.elegans]
129912	AA047344	2	ESTs ESTs; Weakly similar to sirilar to WW/rsp5/WWP domain containing proteins [C.elegans]
104927	AA058855	2	ESTs ESTs; Weakly similar to sirilar to WW/rsp5/WWP domain containing proteins [C.elegans]
132821	AA070724	2	ESTs ESTs; Weakly similar to sirilar to WW/rsp5/WWP domain containing proteins [C.elegans]
108409	AA075578	2	ESTs ESTs; Weakly similar to sirilar to WW/rsp5/WWP domain containing proteins [C.elegans]

*FIG.\_9Ab*

NEW KEY NUMBER	ACCESSION	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE DESCRIPTOR
133621	AA076138	2	H2A histone family; member Y ATPase; Ca++ transporting; cardiac muscle; slow twitch 2 ESTs
108565	AA085342	2	Other TM
104977	AA088228	2	Other Other
103777	AA093131	2	Other Other
108649	AA112540	2	Other Other
114692	AA121995	2	Other Other
105063	AA134985	2	ESTs
133273	AA147725	2	dendritic cell protein ESTs; Highly similar to the KIAA0195 gene is expressed ubiquitously. [H.sapiens]
128515	AA149044	2	ESTs; Weakly similar to Yd372cp [S.cerevisiae] ESTs
105182	AA191014	2	Other Other
109277	AA196332	2	Other Other
132608	AA199588	2	Other Other
109380	AA219015	2	Other Other
130800	AA223386	2	Other Other
129945	AA232104	2	Other Other
105305	AA233609	2	ESTs
128924	AA234962	2	spindle pole body protein ESTs
114895	AA236177	2	Other TM
			Homo sapiens mRNA for KIAA0887 protein; partial cds Other

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FIG.\_9Ac

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
2451	52.6	M21305 AA411502	Human alpha satellite and satellite 3 junction DNA sequence ESTs; Weakly similar to serine protease [H.sapiens]
27090	7.4	D13666	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)
232	7	AA102520	ESTs; Weakly similar to heat shock protein hsp4 homolog [H.sapiens]
25461	6.8		
27665	6.2	AA453783 ESTs	other
39492	6.2	F13673 ESTs	other
28050	5.6	AA489057 ESTs	?
31485	5.6	N71781 ESTs	other
25606	5.4	AA132514 density-regulated protein	other
7000	5	Z74616 collagen; type I; alpha 2	SS
25931	4.7	AA236200 ESTs	other
12118	4.5	AA291528 ESTs	other
32913	4.4	W46810 ESTs	other
26864	4.3	AA393804 R79392	other
22514	4.2	R79392 ESTs	other
25466	4.2	AA112012 lactate dehydrogenase A	TM
32276	4.1	R92994 matrix metalloproteinase 12 (macrophage elastase)	SS
32465	4.1	T32108 ESTs	other
22430	4	R71082 TFAR19 novel apoptosis-related gene	other
30052	4	N32586 ESTs; Weakly similar to Ydr339cp [S.cerevisiae]	other
28354	3.9	C14037 ESTs; Weakly similar to Yel7c-ap [S.cerevisiae]	?
29604	3.9	H98655 Homo sapiens gene for NB31; complete cds	TM
27592	3.8	AA449417 Homo sapiens mRNA for putative glucosyltransferase; partial cds	TM
28691	3.8	D51276 STATHMIN	other
19100	3.7	H10933 ESTs	other

FIG.- 10Aa

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
5891 12288	3.5 3.5	X60486 AA398243	H4 histone family; member G ESTs; Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae:]
23629	3.5	T88700	ESTs; Weakly similar to DFS7 [H.sapiens]
25951	3.5	AA236672	Human mRNA for calgizzain; complete cds
477	3.4	D38583	ESTs
11193	3.4	AA186897	Homo sapiens secreted cement gland protein XAG-2
27193	3.4	AA421562	homolog (hAG-2/R)
32899	3.4	W45728	ESTs; Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPPR
9576	3.3	J03464	collagen; type I; alpha 2
10506	3.3	AA027086	ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN UBP5-SPT
22064	3.3	R51309	ESTs
39217	3.3	C21242	calponin 2
2613	3.2	M29540	CARCINOEMBRYONIC ANTIGEN PRECURSOR
27583	3.2	AA449068	ESTs
40031	3.2	H83442	catechol-O-methyltransferase
10131	3.1	R56183	eukaryotic translation initiation factor 3; subunit 6 (48kD)
25154	3.1	AA043353	ESTs; Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1
25821	3.1	AA164643	ESTs; Weakly similar to Ki-1/57 intracellular antigen [H.sapiens]
26004	3.1	AA243297	ESTs; Weakly similar to PEANUT PROTEIN [Drosophila melanogaster]
27055	3.1	AA406542	ESTs

**FIG.- 10Ab**

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
10844	3	AA1000719	non-specific cross reacting antigen
11358	3	AA232104	ESTs
17389	3	AA121315	ESTs
17415	3	AA122386	"Collagen, type V, alpha 2"
23772	3	T92735	ESTs
25331	3	AA070947	tropomyosin 4
25358	3	AA076138	histone macroH2A1.2
27039	3	AA406145	ESTs
27261	3	AA425544	Homo sapiens clone 2368S mRNA; complete cds
28795	3	D80946	SFRS protein kinase 1
32192	3	R67275	collagen; type XI; alpha 1
3083	2.9	M77349	transforming growth factor; beta induced; 68kD
5519	2.9	X06700	collagen; type III; alpha 1 ( Ehlers-Danlos syndrome type IV; autosomal dominant)
5562	2.9	X12876	keratin 18
11618	2.9	AA251902	Homo sapiens lysophospholipase (LPL 1) mRNA; complete cds
17686	2.9	AA147725	Homo sapiens GA17 protein mRNA; complete cds
18024	2.9	AA188378	ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
20941	2.9	N90933	ESTs
13612	2.8	AA458899	ESTs; Highly similar to (define not available 412715) [H.sapiens]
17799	2.8	AA157818	Human endogenous retroviral protease mRNA; complete cds
25344	2.8	AA075182	Sjogren syndrome antigen A2 (6kD; ribonucleoprotein autoantigen SS-A/R)
25583	2.8	AA131162	ESTs
32170	2.8	R61297	eukaryotic translation initiation factor 3; subunit 6 (48kD)
33586	2.8	Z38656	coatomer protein complex; subunit alpha

**FIG.- 10Ac**

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
2396	2.7	M18728	non-specific cross reacting antigen
3251	2.7	M93036	membrane component; chromosomal 4; surface marker (35kD glycoprotein)
8158	2.7	AA372630	Homo sapiens GW112 protein (GW112) mRNA; complete cds
9207	2.7	D79052	ESTs; Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 GAMM
15051	2.7	U64661	Human poly(A)-binding protein processed pseudogene3 ESTs; Moderately similar to !!! ALU SUBFAMILY SP
15614	2.7	W63627	WARNING ENTRY !!
25323	2.7	AA070485	Homo sapiens clone 23967 unknown mRNA; partial cds
25329	2.7	AA070827	ESTs; Weakly similar to KIAA18 [H.sapiens]
25549	2.7	AA127058	ESTs; Weakly similar to predicted using Genefinder [C.elegans]
25584	2.7	AA131165	heterogeneous nuclear ribonucleoprotein A2/B1
27468	2.7	AA441971	Homo sapiens mRNA for KIAA494 protein; complete cds
32012	2.7	R31180	ESTs
38087	2.7	AA488991	Homo sapiens chaperonin containing t-complex polypeptide 1; beta subunit
38457	2.7	AA598714	Lon protease-like protein
39421	2.7	F03974	H.sapiens mRNA for Sop2p-like protein
3758	2.6	U09587	glycy-tRNA synthetase
8952	2.6	C00038	ESTs
12978	2.6	AA431191	ESTs
17627	2.6	AA135894	"Homo sapiens putative G protein-coupled receptor (RAIG1), Retinoic acid i ESTs; Weakly similar to neogenin [H.sapiens]
20752	2.6	N68921	ESTs
22954	2.6	T17185	ESTs
25808	2.6	AA161161	ESTs

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
27169	2.6	AA418879	proteasome (prosome; micropain) 26S subunit; non-ATPase; 11 ESTs; Moderately similar to ubiquitous TPR motif; Y isoform [H.sapiens] ESTs
28096	2.6	AA490962	ESTs; other
28705	2.6	D54289	ESTs; TM
33593	2.6	Z39041	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE E2F transcription factor 5; p13-binding ESTs
37363	2.6	AA455521	"HUMGS972 Human promyelocyte Homo sapiens cDNA clone pm2344 3', H2A histone family; member Z heterogeneus nuclear ribonucleoprotein A1
39170	2.6	C15324	Homo sapiens mRNA for $\beta$ -aminoimidazole-4-carboxamide-1-beta-D-ribon ESTs; Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MR
39251	2.6	D20002	Homo sapiens androgen receptor associated protein 24 (ARA24) mRNA; c ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sa]
2767	2.5	M37583	lysozyme (renal amyloidosis)
5468	2.5	X04347	histone macroH2A1.2
9243	2.5	D82348	replication protein A3 (14kD)
14791	2.5	T35725	TM
14804	2.5	T48195	SS
16974	2.5	AA070724	other
20031	2.5	N21085	other
25484	2.5	AA112679	?
26830	2.5	AA347359	
28068	2.5	AA490212	
30071	2.5	N33011	

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	
32740	2.5	W31600 AA416785	von Hippel-L heterogeneo
35870	2.5	T59161	Thymosin; b proteasome
41908	2.5	X66401	(large multifl ESTs; Weak)
6011	2.4		ESTs; Weak
9201	2.4	D63079	REDUCTASE  ESTs
9218	2.4	D79891 R32993	ESTs; Highly CYTOPLASI
10085	2.4		DEK gene
10253	2.4	R82411	ESTs; Model
11107	2.4	AA159501	ESTs; Weak
11846	2.4	AA262969	L8167.12 liki
12767	2.4	AA424346	ESTs; Weak
13772	2.4	AA464708	UROIIIS [H.: ESTs; Weak]
16728	2.4	AA053102	exon 13A [H. sa cadherin 17; Li cadherin (liver-intestine)
17774	2.4	AA156243	ESTs; Highly similar to (defline not available 412715) [H.sapiens]
21386	2.4	R24059	ESTs
25433	2.4	AA099589	GDP dissociation inhibitor 2
25603	2.4	AA132032	Homo sapiens CAGH1a (CAGH1) mRNA; partial cds
25791	2.4	AA159980	ELKL motif kinase
26153	2.4	AA252627	ESTs
26852	2.4	AA365527	Weakly similar to TLS-associated protein TASR [H.sapiens] other

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR
27122	2.4	AA416877	ESTs actin; gamma 1
28365	2.4	C14090	Homo sapiens DNA from chromosome 19-cosmid R3879
28626	2.4	D25560	other other other
28687	2.4	D51241	containing USF2; Homo sapiens mRNA for putative vacuolar proton ATPase membrane sect
29850	2.4	N24968	SS,TM vacuolar H(+)-ATPase subunit
32892	2.4	W45457	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]
33811	2.4	AA173143	other other other other
40121	2.4	H93492	ESTs; Highly similar to villin [H.sapiens]
40141	2.4	H94877	ESTs; Moderately similar to putative G-binding protein [H.sapiens]
40167	2.4	H96237	other other other other other
446	2.3	D38073	minichromosome maintenance deficient (S. cerevisiae) 3
3530	2.3	S81914	DIFFERENTIATION-DEPENDENT GENE 2
7835	2.3	AA252436	Homo sapiens lysophospholipase (LPL1) mRNA; complete cds
10898	2.3	AA121879	proteasome (prosome; macropain) subunit; beta type; 9 (large multifunction
10965	2.3	AA134138	ESTs; Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]
11015	2.3	AA143763	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 other
11895	2.3	AA279420	suppressor [C] ESTs; Highly similar to (defline not available 433735) [H.sapiens]
13386	2.3	AA451676	TM other
15464	2.3	W28391	other
17619	2.3	AA135406	other

*FIG.- 10Ag*

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
18225 20450	2.3 2.3	AA213696 N53927	ESTs; Weakly similar to $\alpha$ -phenylalkylamine binding protein [H.sapiens]	other ?
25308	2.3	AA065227	ESTs; Weakly similar to coded for by <i>C. elegans</i> cDNA Yk1c1.3 [C.elegans]	other
26590 27624 27792	2.3 2.3 2.3	AA282151 AA452112 AA460359	ESTs; Weakly similar using Genefinder [C.elegans] Homo sapiens mRNA for putative thioredoxin-like protein ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE II 14 kD?	other other ?
28231 28722 30363 32928	2.3 2.3 2.3 2.3	AA600153 D59711 N47956 W47620	DEK gene ESTs eukaryotic translation initiation factor 3; subunit 3 (gamma; 4kD) ESTs; Weakly similar to reverse transcriptase related protein [H.sapiens]	other other other other
39585 40175 40366 40733 4918 5165 12242 13154	2.3 2.3 2.3 2.3 2.2 2.2 2.2 2.2	H11320 H96665 N26691 N67422 U68105 U81607 AA372018 AA442768	Homo sapiens HRIHFB2 15 mRNA; partial cds peptidylprolyl isomerase B (cyclophilin B) ESTs; Highly similar to (offline not available 467914) [H.sapiens] ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens] poly(A)-binding protein-like 1 GRAVIN ESTs Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23)	TM other other other other other other ?
14276 15721 20588 24021 24250	2.2 2.2 2.2 2.2 2.2	AA598450 W95348 N62945 W42957 W84712	ESTs ESTs Homo sapiens hMmTRA1b mRNA; complete cds ESTs calumenin	other TM TM other other

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
25245	2.2	AA055768	ESTs; SPLICING FACTOR U2AF 35 KD SUBUNIT
25430	2.2	AA099429	heterogeneous nuclear ribonucleoprotein U (scaffold)
25562	2.2	AA128904	attachment factor A)
28745	2.2	D60485	caldesmon 1
31997	2.2	R20669	tumor rejection antigen (ip96) 1
32491	2.2	T47333	Human TFIID subunit TAI=II55 (TAFII55) mRNA; complete cds
32636	2.2	T93807	high-mobility group (nonhistone chromosomal) protein 1
37703	2.2	AA476237	ESTs; Weakly similar to uroporphyrinogen III synthase; UROIII [H.sapien]
215	2.1	D13627	Human mRNA for KIAA2 gene; complete cds
2449	2.1	M21259	small nuclear ribonucleoprotein polypeptide E
3205	2.1	M88458	ER LUMEN PROTEIN RETAINING RECEPTOR 2
4197	2.1	U31556	E2F transcription factor 5; p13-binding
4811	2.1	U62962	eukaryotic translation initiation factor 3; subunit 6 (48kD)
5417	2.1	X01060	transferrin receptor (p9; CD71)
6334	2.1	X83228	cadherin 17; LI cadherin (liver-intestine)
6605	2.1	X99133	NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR
10471	2.1	AA024482	ESTs; Highly similar to KERATIN; TYPE I CYTOSKELETAL other
11027	2.1	AA148318	14 [Homo sa] Human mRNA for KIAA65 gene; partial cds
11116	2.1	AA161292	INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN
11540	2.1	AA236972	ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!
11937	2.1	AA280865	ESTs; Weakly similar to Similarity to Yeast hypothetical protein YOR316O

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
17312	2.1	AA111889 H18947 N26259	pigment epithelium-derived factor ESTs ESTs; Weakly similar to uroporphyrinogen III synthase; UROIIIS [H.sapien]
19286	2.1	N91492 N98464 AA412452 AA488433	Homo sapiens clone 628 unknown mRNA; complete sequence ESTs ESTs ESTs; Weakly similar to cleduced amino acid sequence is highly homologous
20122	2.1	AA521256	ESTs; Highly similar to nuclear pore complex protein NUP17 [R.norvegicus]
20946	2.1	AA621604 D59570	ESTs ESTs
20997	2.1	F04674 R48608 W90444 W96151	Homo sapiens mRNA for KIAA746 protein; partial cds eukaryotic translation initiation factor 3, subunit 7 (zeta; 66/67kD) ESTs; Highly similar to (define not available 4454524) [H.sapiens] ESTs; Moderately similar to ganglioside-induced differentiation associated
27106	2.1	AA412270 AA608751 D57317 H73484	ESTs cathepsin B Human transcriptional co-activator PC4 mRNA; complete cds ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like
28036	2.1	H78323	Homo sapiens E2F-related transcription factor (DP-1) mRNA; complete cds
28167	2.1	N27198	ESTs
28336	2.1		other
28719	2.1		other
28886	2.1		other
32124	2.1		other
33433	2.1		other
33564	2.1		?
35778	2.1		other
38588	2.1		SS
39301	2.1		SS,TM
39945	2.1		other
39977	2.1		other
40376	2.1		other

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	
41795	2.1	T28799	ESTs; Highly similar to TYROSINE-PROTEIN KINASE RECEPTOR EPH-RECEPTOR EPH-	TM
1714	2	L09604	proteolipid protein 2 (colonic epithelium-enriched)	TM
2001	2	L33930	"Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region	TM
3278	2	M94556	single-stranded DNA-binding protein	other
4145	2	U28749	high-mobility group (nonhistone chromosomal) protein isoform I-C	TM
8149	2	AA364267	ESTs; Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN C	other
9844	2	N33807	ESTs; Highly similar to NEDD-4 PROTEIN [Homo sapiens]	other
14032	2	AA486092	ESTs; Weakly similar to CH-TOG PROTEIN [H.sapiens]	TM
16395	2	AA025673	ESTs; Moderately similar to (define not available 416878) [H.sapiens]	TM
17327	2	AA112540	ESTs	TM
23083	2	T30881	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	other
25625	2	AA133969	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	other
28073	2	AA490494	ESTs	other
28700	2	D53139	ribosomal protein S28	other
29095	2	H27188	collagen-binding protein 2 (collagen 2)	other
32191	2	R67083	calnexin	SS,TM
32897	2	W45664	5' nucleotidase (CD73)	other
10782	1.6	AA074880	ESTs; Weakly similar to HYPOTHETICAL 85. KD PROTEIN IN CPA2-ATP	other
27795	1.6	AA460454	ESTs; Weakly similar to KIAA512 protein [H.sapiens]	other

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
28706	1.6	D54296	Human mRNA for KIAA255 gene; complete cds TM
36414	1.6	AA430186	ESTs other
9979	1.5	N91087	ESTs; Weakly similar to F55A12.9 [C.elegans] other
9987	1.5	N95507	ESTs; Weakly similar to KIAA319 [H.sapiens] TM
10656	1.5	AA047290	ESTs other
14977	1.5	U37546	apoptosis inhibitor 1 TM
27065	1.5	AA410294	Human mRNA for KIAA336 gene; complete cds other
29278	1.5	H72948	biglycan SS
31917	1.5	N98238	ESTs other
38272	1.5	AA496533	ESTs other
41396	1.5	R55342	CD68 antigen other
41966	1.5	T67710	ESTs ?
8439	1.4	AA436304	Homo sapiens androgen receptor associated protein 24 (ARA24) mRNA; c other
10311	1.4	AA001936	ESTs other
10859	1.4	AA112149	ESTs other
11279	1.4	AA213410	ESTs SS
13548	1.4	AA456033	ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN UBP5-SPT other
14340	1.4	AA599653	Homo sapiens TCFL5 mRNA for transcription factor-like 5; complete cds ESTs other
32180	1.4	R63727	ESTs other
35187	1.4	AA398722	ESTs other
37254	1.4	AA453483	ESTs TM
1344	1.3	HG4757-	other
5397	1.3	HT5207	"Oncogene MLL-Af4, Fusion Activated"
		V01516	KERATIN; TYPE II CYTOSKELETAL 6D SS,TM

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
16272	1.3	AA018922	core promoter element binding protein
23427	1.3	T70356	ESTs; Highly similar to 2'OL POLYPROTEIN [Simian sarcoma virus]
25718	1.3	AA150741	gene with multiple splice variants near HD locus on 4p16.3
33499	1.3	W93403	ESTs
36574	1.3	AA434454	ESTs; Weakly similar to off; hypothetical protein [E.coli]
41548	1.3	R82846	ESTs
2386	1.2	M17863	insulin-like growth factor 2 (somatomedin A)
6388	1.2	X86371	lethal giant larvae ( <i>Drosophila</i> ) homolog 1
24427	1.2	Z38208	ESTs
27089	1.2	AA411473	adducin 1 (alpha)
33177	1.2	W73195	ESTs
34852	1.2	AA347691	ESTs
35325	1.2	AA400273	ESTs
36609	1.2	AA435668	ESTs; Weakly similar to putative p15 [H.sapiens]
38477	1.2	AA598939	ESTs
40975	1.2	R02547	ESTs
41874	1.2	T51150	ESTs
8235	1.1	AA401047	Homo sapiens mRNA for neuropeptin; complete cds
9772	1.1	M81349	SERUM AMYLOID A-4 PROTEIN PRECURSOR
14758	1.1	SS83198	BPLP
15831	1.1	X90579	H.sapiens DNA for cyp related pseudogene
20656	1.1	N66289	ESTs
24891	1.1	AA004502	cerebroside (3'-phosphoadenylsulfate:galactosylceramide 3')
			sulfotransfer
29045	1.1	H13649	ESTs
31584	1.1	N74690	ESTs

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
31640	1.1	N78784	Homo sapiens BimEL mRNA; complete cds
35293	1.1	AA400013	EST
37583	1.1	AA461499	ESTs
37852	1.1	AA479896	ESTs
38397	1.1	AA521342	ESTs
38652	1.1	AA609018	ESTs
40397	1.1	N29963	ESTs; Moderately similar to !!! ALU CLASS C WARNING ENTRY !!! [H.sa]
40488	1.1	N40559	ESTs; Highly similar to LEUKOTOXIN SECRETION ATP-BINDING PROT
41231	1.1	R41772	EST
41333	1.1	R48580	ESTs
3255	1	M93143	"Homo sapiens plasmirogen-like protein (PLGL) mRNA, complete cds"
5742	1	X53065	Accession not listed in Genbank
6007	1	X66363	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1
15233	1	W04960	ESTs
15262	1	W17304	Homo sapiens mRNA for KIAA97 protein; complete cds
15363	1	W26847	ESTs; Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MS
15606	1	W58725	mitogen-activated protein kinase-activated protein kinase 2
18435	1	AA233898	ESTs
21736	1	R41999	ESTs
25306	1	AA065081	"Zm13a3.s1 Stratagene pancreas (#93728) Homo sapiens cDNA clone IMA
29111	1	H40486	ESTs; Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.s]

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
34743	1	AA302772	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]
34801	1	AA342526	ESTs; Moderately similar to unknown [H.sapiens]
35355	1	AA400521	other
36940	1	AA446449	other
39221	1	C21330	other
1322	0.9	HG4535-	other
		Dematin	
9982	0.9	HT4940	
10084	0.9	N94146	other
11701	0.9	R32932	other
12088	0.9	AA255546	other
15267	0.9	AA287566	other
15901	0.9	W19098	other
21906	0.9	Z20905	SS
22002	0.9	R45512	other
23136	0.9	R49459	other
28673	0.9	T40827	other
29159	0.9	D45719	other
32610	0.9	H60824	other
32674	0.9	T89122	SS,TM
35426	0.9	W02129	other
38504	0.9	AA401409	other
		AA599209	other
244	0.8	D14446	TM
14204	0.8	AA496980	other
25250	0.8	AA056210	other
9971	0.7	N87590	other
		ESTs	
		fibrinogen-like 1	

FIG.- 10A0

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NEW KEY NUMBER	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR
20461	0.7	N54429 R08615	ESTs homogentisate 1;2-dioxogenase (homogentisate oxidase)
41029	0.7	T71012	fibrinogen; B beta polypeptide
41985	0.6		other other SS, TM

*FIG.\_10Ap*

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				TM	SS
134804	12.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	TM	TM
130617	11.4	M90516	glutamine-fructose-6-phosphate transaminase 1	TM	TM
104209	10.6	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated	SS	SS
109991	10	H09813	ESTs	TM	TM
124315	8.3	H94892	v-ras simian leukemia viral oncogene homolog A (ras related)	Other	Other
132977	8.2	U28686	RNA binding motif protein 3	Other	Other
130407	7.4	N29888	ESTs; Weakly similar to KIAA0226 [H.sapiens]	Other	Other
116176	6.6	AA463725	ESTs	Other	Other
119271	6.5	T16387	cytochrome b-245; beta polypeptide (chronic	TM	TM
134711	6.5	X04011	granulomatous disease)	Other	Other
134326	6.1	U16306	"Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds"	Other	Other
125852	5.9	H09290	ESTs; Weakly similar to unknown [H.sapiens]	SS, TM	SS, TM
112169	5.9	R48589	ESTs	TM	TM
132528	5.9	AA283006	chromosome-associated polypeptide C	Other	Other
134367	5.7	X54199	phosphoribosylglycinamide formyltransferase; phosphoribosylaminoimidazole synthetase;	Other	Other
111929	5.2	R40057	prominin (mouse)-like 1	SS, TM	SS, TM
102165	5	U18321	Death associated protein 3	Other	Other
130441	5	U35835	protein kinase; DNA-activated; catalytic polypeptide	Other	Other
133282	5	U52960	SRB7 (suppressor of RNA polymerase B; yeast) homolog	Other	Other
100783	4.9	HG3748-	"Basic Transcription Factor, 44 Kda Subunit"	Other	Other
		HT4018			

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	ESTs
122223	4.9	AA436158	ESTs	Other	SS
104660	4.8	AA007160	ESTs	Other	Other
113702	4.8	T97307	ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING ENTR Y !!! [H.sapiens]		
101185	4.7	L19872	ESTs	Other	Other
105308	4.7	AA233744	ESTs	Other	Other
107168	4.7	AA621540	ESTs	Other	SS
101201	4.6	L22524	matrix metalloproteinase 7 (matrilysin; uterine)	TM	
101809	4.5	M86849	"Homo sapiens connexin 26 (GJB2) mRNA, complete cds"	Other	Other
101478	4.5	M23379	RAS p21 protein activator (GTPase activating protein) 1	Other	Other
104695	4.5	AA012953	mesoderm specific transcript (mouse) homolog	TM	TM
100365	4.4	D78611	"EST176522 Colon carcinoma (Caco-2) cell line II Homo	Other	Other
126819	4.3	AA305536	sapiens cDNA 5' end, mRNA sequence."		
1011880	4.3	M97925	defensin; alpha 5; Paneth cell-specific	SS	
126838	4.2	AA858097	pigment epithelium-derived factor	Other	Other
101684	4.2	M63256	cerebellar degeneration-related protein (62kD)	Other	Other
117634	4.2	N36421	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTR Y !!! [H.sapiens]	Other	Other
132109	4.1	AA599801	ESTs	Other	Other
115054	4.1	AA252863	ESTs	Other	Other
106553	4	AA454967	ESTs	Other	Other
119717	3.9	W69134	ESTs	Other	Other
131945	3.9	M87339	replication factor C (activator 1) 4 (37kD)	Other	Other
128790	3.9	AA291725	secreted frizzled-related protein 4	SS	SS
120562	3.8	AA280036	ESTs; Weakly similar to W01A6.c [C.elegans]	Other	Other
109517	3.7	D60799	ESTs		

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**FIG.\_ 11Ab**

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	SS Other Other
102618	3.7	U65932 AA434441 D83004	extracellular matrix protein 1 frizzled (Drosophila) homolog 7 ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	ESTs	SS Other Other
106286	3.7		platelet-activating factor acetylhydrolase; isoform 1b; gamma subunit (29kD)		
133640	3.6	D63391			
100335	3.6				
104720	3.6	AA018441 U43701 AA236324	ribosomal protein L23a ESTs; Weakly similar to !!! ALU CLASS A WARNING ENTRY !!! [H.sapiens]	ESTs	Other Other SS
107348	3.6				
134989	3.6				
111345	3.6	N89820 AA600147	ESTs; Weakly similar to Similar to NADH-cytochrome B5 reductase [C.elegans]	ESTs	Other Other
107053	3.6				
107240	3.5	D59368 AA620553 AA431505 S58544 AA621169 AA411621 S79219 H64938 AA937173 AA478587	flap structure-specific endonuclease 1 Homo sapiens mRNA for putative Sqv-7-like protein; partial sperm associated antigen ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	Other Other TM Other Other Other Other Other Other Other Other Other Other Other	
107129	3.5				
134846	3.5				
101897	3.5				
107151	3.5				
106012	3.4				
101950	3.4				
116844	3.4				
128025	3.4				
106785	3.4				
104518	3.4	R09815	leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL) proteasome (prosome; macropain) 26S subunit; ATPase; 5	ESTs	Other Other
117667	3.4	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase		Other Other

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO		
				ESTs; Moderately similar to (defline not available 4753768)	ESTs; [H.sapiens]	Other
104954	3.3	AA074514	ESTs; Moderately similar to (defline not available 4753768)			
105372	3.3	AA236481	ESTs; [H.sapiens]		Other	
104896	3.3	AA054228	ESTs; [H.sapiens]		Other	
113485	3.3	T87863	ESTs; [H.sapiens]		Other	
127003	3.3	AA550806	ESTs; Weakly similar to (defline not available 3882151) [H.sapiens]		Other	TM
100305	3.3	D50487	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)	SS		
134722	3.2	W47183	ESTs; Weakly similar to !!! ALU SUBFAMILY SB2 WARNING ENTRY !!! [H.sapiens]	Other		
126801	3.2	AA512902	ESTs; Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	SS, TM		
133503	3.2	M33195	ESTs; Human MAC30 mRNA; 3' end	SS, TM		
132183	3.2	L19183	ESTs; ENTRYS; Moderately similar to !!! ALU SUBFAMILY SP WARNING	TM		
105298	3.2	AA233459	ESTs; ENTRYS; Moderately similar to !!! ALU SUBFAMILY SP WARNING	TM		
111046	3.2	N55514	ESTs; ENTRYS; Moderately similar to !!! ALU SUBFAMILY SP WARNING	TM		
135309	3.2	D25984	ESTs; nuclear RNA helicase; DEC:D variant of DEAD box family	SS		
102808	3.2	U90426	ESTs; "Protein Kinase Ht31, Cam>-Dependent"	Other		
100552	3.1	HG2167-HT2237	ESTs; ESTs; "Protein Kinase Ht31, Cam>-Dependent"	Other		
127652	3.1	AA804487	ESTs; ESTs; "Protein Kinase Ht31, Cam>-Dependent"	Other		
116127	3.1	AA459703	ESTs; CEESD64F [C.elegans]	TM		
131904	3.1	AA143019	ESTs; Highly similar to surface 4 integral membrane protein [H.sapiens]	TM		
126547	3.1	U47732	transmembrane 4 superfamily member 3	Other		
102823	3.1	U90914	carboxypeptidase D	SS		

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				Other	SS, TM
132298	3.1	N41849	Homo sapiens cytokine receptor related protein 4 (CYTGOR4) mRNA; complete cds	ESTs	Other
127445	3.1	AA906286	lysosomal-associated membrane protein 2 ESTs; Weakly similar to semaphorin C [M.musculus]	ESTs	Other
134395	3.1	L09717	"YY1 transcription factor	ESTs	Other
105743	3.1	AA293300	cytidine deaminase	ESTs	Other
125827	3.1	AI471525	defensin; alpha 6; Paneth cell-specific	ESTs	Other
101229	3.1	L27943	"yc82f8.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:2242 5'; mRNA sequence"	ESTs	Other
102306	3	U33317	EST	ESTs	TM
107318	3	T74445	gogi SNAP receptor complex member 1 ESTs	ESTs	SS
120983	3	AA398209	"HUM272B04B Human aorta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-272B04 5'; mRNA sequence."	ESTs	Other
134700	3	AA481414	ESTs	ESTs	Other
131216	3	D31058	TS translation elongation factor; mitochondrial	ESTs	Other
127565	3	D79516	ESTs	ESTs	Other
106882	2.9	AA489009	"yr73g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:21(960 5', mRNA sequence."	ESTs	Other
130874	2.9	T08287	ESTs	ESTs	Other
101275	2.9	L37936	ESTs	ESTs	Other
111179	2.9	N67239	ESTs	ESTs	Other
126086	2.9	H70975	ESTs	ESTs	Other
105365	2.9	AA236275	ESTs	ESTs	Other
118789	2.9	N75416	H.sapiens PAP mRNA	ESTs	Other
115117	2.9	AA256492	"Guanine Nucleotide-Bir ding Protein Rai, Ras-Oncogene Related"	ESTs	Other
100484	2.9	HG1103- HT1103	Homo sapiens (clone s153) mRNA fragment	ESTs	Other
101300	2.9	L40391			

**FIG.- 11Ae**

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	Other
103075	2.9	X59543	ribonucleotide reductase M1 polypeptide		Other
132164	2.8	U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2		Other
106716	2.8	AA464962			Other
134098	2.8	X06323	Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3		Other
134485	2.8	X82153	cathepsin K (pycnodysostosis)	SS	
129634	2.8	AA150726			Other
112207	2.8	R49602			Other
124904	2.8	R86970			Other
125471	2.8	AA477571	UDP-glucose ceramide glucosyltransferase	SS	
132180	2.8	AA405569	fibroblast activation protein; alpha	SS	
104454	2.8	M84443	galactokinase 2	TM	
134282	2.8	T25508			Other
101558	2.8	M32011	neutrophil cytosolic factor 2 (65kD; chronic granulomatous disease; autosomal 2)		Other
130529	2.8	AA173238	small inducible cytokine A5 (RANTES)		Other
101804	2.7	M86699	TTK protein kinase		Other
109565	2.7	F01930			Other
112427	2.7	R62604			Other
115188	2.7	AA261819			Other
121831	2.7	AA425374			Other
132454	2.7	W78726	ESTs; Highly similar to serine/threonine kinase [H.sapiens]		Other
116399	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds		Other
100409	2.7	D86957	Human mRNA for KIAA0202 gene; partial cds		Other
130987	2.7	R45698			Other
107217	2.7	D51095			SS, TM

**FIG.- 11Af**

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				SS	
125698	2.6	AA748483	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds	SS	Other
118722	2.6	N73563	"yf47c1.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:132 5' mRNA sequence"	ESTs	
104521	2.6	R11604	ESTs; Weakly similar to katanin p80 subunit [H.sapiens] protein tyrosine phosphatase type IVA; member 2	ESTs	Other
130800	2.6	AA223386	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	ESTs	TM
134415	2.6	AA329274	Transcriptional Coactivator Pc4	ESTs	Other
116461	2.6	AA621557	"z143h5.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:54729 5' mRNA sequence"	ESTs	Other
100864	2.6	HG4297-HT4567	"z143h5.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:54729 5' mRNA sequence"	ESTs	Other
103818	2.6	AA150614		ESTs	Other
105713	2.6	AA291321		ESTs	Other
114969	2.6	AA250775		ESTs	Other
130415	2.6	X07290	Human HF.12 gene mRNA	ESTs	Other
101791	2.6	M83822	Human beige-like protein (BGL) mRNA; partial cds	ESTs	Other
128131	2.6	AI283162	claudin 3	ESTs	SS, TM
131564	2.6	AA491465		ESTs	Other
100279	2.6	D42084	Human mRNA for KIAA0094 gene; partial cds	ESTs	Other
130149	2.6	J04031	methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methenyltetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase	ESTs	Other
119888	2.6	W81710		ESTs	SS
126638	2.6	AA649257		ESTs	Other
131672	2.6	X12901	Human mRNA for villin-	ESTs	Other

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE		ORF STRUCTURAL INFO
134405	2.6	J04177	collagen; type XI; alpha 1		Other
101188	2.5	L20320	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)		TM
104534	2.5	R22303	ESTs; Weakly similar to putative p150 [H.sapiens]		Other
135179	2.5	U43747	Friedreich ataxia		SS
124308	2.5	H93575			SS
125621	2.5	AI051602	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)		TM
101342	2.5	L76191	interleukin-1 receptor-associated kinase 1		Other
129351	2.5	AA167268	ESTs		Other
103774	2.5	AA092898	ESTs; Weakly similar to R07G3.8 [C.elegans]		Other
131289	2.5	AA485697	ESTs		SS, TM
132094	2.5	W01996	ESTs; Highly similar to (define not available 4929683) [H.sapiens]		Other
103223	2.5	X74801	chaperonin containing TCP1; subunit 3 (gamma)		Other
105610	2.5	AA279991	ESTs		Other
115719	2.5	AA416997	ESTs		Other
134888	2.5	AA148094	Tat-interacting protein (30kD)		Other
105564	2.5	AA262943	ESTs		Other
129689	2.5	AA130156	ESTs		Other
103391	2.5	X94453	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)		Other
104182	2.5	AA479990	ESTs; Weakly similar to glicma amplified on chromosome 1 protein [H.sapiens]		SS, TM
123494	2.5	AA599786	ESTs		Other
122905	2.5	AA470070	ESTs		Other
109175	2.5	AA180496	ESTs		Other

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	Other
129907	2.5	D80170	ESTs; Weakly similar to !!! ALU SUBFAMILY SQ WARNING	Other	Other
115142	2.4	AA258116	ENTRY !!! [H.sapiens]	Other	Other
125474	2.4	AA151216	Homo sapiens 14-3-3 protein mRNA; complete cds	SS	Other
125745	2.4	AI283493	ribophorin II	Other	Other
100103	2.4	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit	Other	Other
102687	2.4	U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Other	Other
133170	2.4	U21049	epithelial protein up-regulated in carcinoma	SS, TM	Other
109141	2.4	AA176428	ESTs	Other	Other
132811	2.4	U25435	transcriptional repressor	SS, TM	Other
102862	2.4	X01057	interleukin 2 receptor; alpha	Other	Other
104300	2.4	D37933	syntaxin 1B	Other	Other
105091	2.4	AA148859	ESTs; Moderately similar to !!! ALU SUBFAMILY J	Other	Other
110674	2.4	H89315	WARNING ENTRY !!! [H.sapiens] "yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253288 3', mRNA sequence."	TM	Other
122571	2.4	AA452600	EST	Other	Other
123421	2.4	AA598440	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	Other	Other
132181	2.4	AA046939	ESTs; Moderately similar to !!! ALU SUBFAMILY SX	Other	Other
129445	2.4	AA306121	WARNING ENTRY !!! [H.sapiens]	SS	Other
113923	2.4	W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]	Other	Other

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO		
				+	+	+
100598	2.4	HG2463- HT2559	Guanine Nucleotide-Binding Protein G25k	Other	Other	Other
130869	2.4	AA128100	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ	Other	Other
132393	2.4	W85888	WARNING ENTRY !!! [H.sapiens]	Rad2	Other	Other
100830	2.4	HG4074- HT4344	cadherin 11 (OB-cadherin; osteoblast) Transketolase-Like Protein	D21255 HG4316- HT4586	ESTs	SS, TM Other
133765	2.4	W80702	YY1 transcription factor	M77698	ESTs; Weakly similar to (defline not available 3874821)	Other
100867	2.4	AA258030	[C.elegans]	AA258030	KIAA0175 gene product	Other
119859	2.4	U18291	CDC16 (cell division cycle 16; <i>S. cerevisiae</i> ; homolog)	D79997	ESTs	Other
135269	2.4	AA521157	KIAA0175 gene product	AA521157	ESTs	TM
115140	2.4	AA234717		AA459956	ESTs	Other
102162	2.4	AA436475		AA436475	ESTs	Other
100372	2.4	T62771	Homo sapiens nucleoplasmmin-3 (NPM3) mRNA; complete cds	T69868	ESTs	Other
106981	2.4	T69868	chaperonin containing TCF 1; subunit 2 (beta)	AB000584	ESTs	SS
130114	2.4	AB000584	prostate differentiation factor	Y13936	ESTs	Other
116129	2.3	Y13936	protein phosphatase 1 G (formerly 2C); magnesium-dependent; gamma isoform	AA730136	ESTs	Other
122235	2.3	AA730136	teratocarcinoma-derived growth factor 1			
107315	2.3					
125905	2.3					
133061	2.3					
107531	2.3					
125820	2.3					

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTS;	Other
131725	2.3	AA456264	ESTS; Highly similar to (clefline not available 4176448) [H.sapiens] chaperonin containing TCP1; subunit 6A (zeta 1)	Other	Other
101228	2.3	L27706	ESTS; Highly similar to (clefline not available 4809026) [H.sapiens]	SS, TM	Other
132571	2.3	R84594	"Human BAC clone RG367O17 from 7p15-p21, complete sequence [Homo sapiens]"	Other	Other
100090	2.3	AC002486		SS	SS
103658	2.3	Z74615	collagen; type I; alpha 1	TM	Other
104897	2.3	AA054641	ESTS	Other	Other
106818	2.3	AA480890	ESTS	Other	Other
113077	2.3	T40442	ESTS	SS	SS
128773	2.3	M28879	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)		
129506	2.3	AA258286	Homo sapiens mRNA for KIAA0877 protein; partial cds	TM	Other
133746	2.3	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	Other	Other
134272	2.3	X76040	Lon protease-like protein	Other	Other
106267	2.3	AA431873	Homo sapiens clone 24711 mRNA sequence	Other	Other
133493	2.3	AA284143	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA; complete cds	Other	Other
104278	2.3	C02582	ESTS; Highly similar to (clefline not available 5114045) [H.sapiens] "aa28c03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564 5', mRNA/ sequence."	Other	Other
127211	2.3	AA480935		Other	Other
110721	2.3	H97678	ESTS	Other	TM
114774	2.3	AA150043	ESTS	Other	Other
132968	2.3	N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Other	Other
106916	2.3	AA490814	ESTS	Other	Other
113849	2.3	W60439	ESTS; Moderately similar to cbp146 [M.musculus] CCAAT/enhancer binding protein (C/EBP); gamma	Other	Other
131028	2.3	U20240		Other	Other

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE			ORF STRUCTURAL INFO
			ESTS	ESTS; Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	ESTS; Moderately similar to unknown protein [H.sapiens]	
130380	2.3	U55853	Homo sapiens 130 kD Gc1g1-localized phosphoprotein (GPP130)	mRNA; complete cds		SS
125390	2.3	H95094	KIAA0016 gene product			SS, TM
127256	2.3	AA327550	ESTS; Weakly similar to !!! ALU SUBFAMILY SQ WARNING			Other
132116	2.3	AA234767	ESTS			SS, TM
117765	2.3	N47797	ESTS			Other
119126	2.3	R45175	ESTS			Other
129482	2.2	AA435849	ESTS; Moderately similar to unknown protein [H.sapiens]			Other
120493	2.2	AA255933	ESTS			SS
108927	2.2	AA143493	ESTS; Weakly similar to PLECKSTRIN [H.sapiens]			Other
122520	2.2	AA449427	ESTS; Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens]			Other
125982	2.2	R98091	RAE1 (RNA export 1; S.pombe) homolog			Other
132325	2.2	N37065	ESTS; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]			Other
100287	2.2	D43950	Human mRNA for KIAA0098 gene; partial cds			Other
114895	2.2	AA236177	Homo sapiens mRNA for KIAA0887 protein; partial cds			Other
105038	2.2	AA130273	ESTS; Weakly similar to (defline not available 4240269) [H.sapiens]			Other
105476	2.2	AA255473	ESTS			SS
106942	2.2	AA496347	ESTS; Highly similar to gene 7442 protein [H.sapiens]			Other
110566	2.2	H59990	ESTS			Other
111068	2.2	N58397	ESTS			Other
127963	2.2	A1299013	"qn13h12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898183 3' similar to TR:O22813 O22813 PUTATIVE NAD (P)-DEPENDENT CHOLESTEROL DEHYDROGENASE. , mRNA sequence."			TM

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	
130985	2.2	AA243700	Homo sapiens mRNA for KIAA0851 protein; complete cds	Other	TM
132877	2.2	R40685	cyclin E1	TM	TM
135242	2.2	M74093	secreted protein; acidic; cysteine-rich (osteonectin)	SS	SS, TM
129468	2.2	J03040	decorin	Other	Other
132616	2.2	AA386264	ESTs	Other	Other
133780	2.2	M14219	ESTs	SS	SS
121853	2.2	AA425887	ESTs	Other	Other
114608	2.2	AA079381	ESTs	SS	SS
129017	2.2	H13108	ESTs	Other	Other
132725	2.2	L41887	splicing factor; arginine/serine-rich 7 (35kD)	ESTs	ESTs
125606	2.2	R28463	ESTs; Highly similar to (define not available 4583654) [H.sapiens]	Other	Other
105538	2.2	AA258860	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other	Other
133221	2.2	AA235289	ESTs	Other	Other
106389	2.2	AA446949	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Other	Other
128949	2.2	AA190993	ESTs	Other	Other
120969	2.2	AA398116	Human mRNA for KIAA0085; gene; partial cds	TM	TM
102495	2.2	U51240	protease inhibitor 3; skin-derived (SKALP)	SS	SS
101124	2.2	L10343	syndecan binding protein (synterin)	Other	Other
102778	2.2	U83463	creatine kinase; mitochondrial 2 (sarcomeric)	Other	Other
107307	2.2	T52099	ESTs	Other	Other
111605	2.2	R11638	arginyl-tRNA synthetase	SS	SS
101959	2.2	S80343	matrix metalloproteinase 9 (gelatinase B; 92kD gelatinase;	Other	Other
101031	2.2	J05070	92kD type IV collagenase)	TM	TM
131701	2.2	AA149008	ESTs; Weakly similar to III ALL SUBFAMILY SQ WARNING G	Other	Other
105344	2.2	AA235303	ENTRY !!! [H.sapiens]	TM	TM

**FIG.- 11Am**

PRIMEKEY	FOLD UPREGULATED INTUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO
103166	2.2	X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Other
131463	2.2	X74142	forkhead (Drosophila)-like 1	Other
131412	2.2	U34044	Human selenium donor protein (selD) mRNA; complete cds	Other
134982	2.2	N46086	ESTs	Other
127236	2.1	AI341818	budding uninhibited by benzimidazoles 1 (yeast homolog)	Other
104459	2.1	M91493	EST	Other
124596	2.1	N70088	ESTs	Other
105650	2.1	AA282347	ESTs; Highly similar to (defline not available 4454694) [H.sapiens]	Other
134917	2.1	X87241	FAT tumor suppressor (Drosophila) homolog	SS
132478	2.1	H20906	Homo sapiens mRNA for KIAA0746 protein; partial cds	SS, TM
134464	2.1	N79354	ESTs; Weakly similar to Rga [D.melanogaster]	Other
111221	2.1	N68869	ESTs	Other
100892	2.1	HG4557-HG4557-HT4962	"Small Nuclear Ribonucleoprotein U1, 1snrp"	Other
111710	2.1	H98153	ESTs	Other
124049	2.1	F10523	primase; polypeptide 2A (58kD)	Other
131692	2.1	D50914	Human mRNA for KIAA0124 gene; partial cds	TM
103003	2.1	X52003	trefoil factor 1 (breast cancer; estrogen-inducible sequence expressed in)	SS
134085	2.1	U20979	chromatin assembly factor 1 (150 kDa)	Other
126216	2.1	N23870	ESTs	Other
102721	2.1	U79241	Human clone 23759 mRNA; partial cds	Other
128040	2.1	AA918528	ESTs	Other
101038	2.1	J05249	replication protein A2 (32kD)	SS
106060	2.1	AA417287	C-terminal binding protein 2	Other
103622	2.1	Z48042	basic transcription factor 3	Other
127884	2.1	AA768630	ESTs	Other

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	STRUCTURAL INFO	
				ORF	ESTIMATE
130911	2.1	W72906	HIRA interacting protein 4 (Inaj-like)	Other	
104260	2.1	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA; complete cds	Other	
120714	2.1	AA292689	ESTs	Other	
101578	2.1	M34423	galactosidase; beta 1 ESTs	SS	
113443	2.1	T86158	Accession not listed in Genbank	SS	
101516	2.1	M28249	ESTs; Moderately similar to !!! ALU SUBFAMILY SB WARNING	Other	
106480	2.1	AA450373	ENTRY !!! [H.sapiens]	Other	
111365	2.1	N92659	ESTs	Other	
121121	2.1	AA399371	ESTs; Weakly similar to (define not available 4688925) [H.sapiens]	Other	
124768	2.1	R40177	ESTs	Other	
102501	2.1	U51586	Human siah binding protein 1 (SiahBP1) mRNA; partial cds	Other	
106432	2.1	AA448850	ESTs	Other	
132812	2.1	R48108	ESTs	TM	
125681	2.1	AA394176	accessory proteins BAP31/E1AP29	Other	
130511	2.1	L32137	cartilage oligomeric matrix protein	Other	
128219	2.1	AA978333	ESTs	Other	
130962	2.1	AA102051	transmembrane 4 superfamily member 6	SS, TM	
101840	2.1	M93056	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	TM	
123928	2.1	AA621363	EST	Other	
132073	2.1	N67408	ESTs; Moderately similar to !!! ALU SUBFAMILY SC WARNING	Other	
			ENTRY !!! [H.sapiens]		
			S-adenosylhomocysteine hydrolase	Other	
101671	2.1	M61832	ESTs	Other	
107059	2.1	AA608545	ESTs	Other	
132791	2.1	AA446088	ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens]	Other	
103131	2.1	X65614	S100 calcium-binding protein P	Other	
104791	2.1	AA029046	ESTs	Other	

**FIG.-11AO**

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				TM	SS
134804	12.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	TM	TM
130617	11.4	M90516	glutamine-fructose-6-phosphate transaminase 1	TM	SS
104209	10.6	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated	Other	Other
109991	10	H09813	ESTs	Other	Other
124315	8.3	H94892	v-ras simian leukemia viral oncogene homolog A (ras related)	Other	Other
132977	8.2	U28686	RNA binding motif protein 3	Other	Other
130407	7.4	N29888	ESTs	Other	Other
116176	6.6	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]	Other	Other
119271	6.5	T16387	cytochrome b-245; beta polypeptide (chronic	TM	TM
134711	6.5	X04011	granulomatous disease)	Other	Other
134326	6.1	U16306	"Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds"	SS, TM	TM
125852	5.9	H09290	ESTs; Weakly similar to unknown [H.sapiens]	Other	Other
112169	5.9	R48589	ESTs	Other	Other
132528	5.9	AA283006	chromosome-associated polypeptide C	Other	Other
134367	5.7	X54199	phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase;	SS, TM	Other
			phosphoribosylaminoimidazole synthetase	Other	Other
111929	5.2	R40057	prominin (mouse)-like 1	Other	Other
102165	5	U18321	Death associated protein 3	Other	Other
130441	5	U35835	protein kinase; DNA-activated; catalytic polypeptide	Other	Other
133282	5	U52960	SRB7 (suppressor of RNA polymerase B; yeast) homolog	Other	Other
100783	4.9	HG3748-	"Basic Transcription Factor; 44 Kda Subunit"	Other	Other
		HT4018			

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	ESTs
122223	4.9	AA436158	ESTs	Other	SS
104660	4.8	AA007160	ESTs	Other	Other
113702	4.8	T97307	ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	Other	Other
101185	4.7	L19872	ESTs	Other	SS
105308	4.7	AA233744	ESTs	Other	Other
107168	4.7	AA621540	ESTs	Other	Other
101201	4.6	L22524	matrix metalloproteinase 7 (matrilysin; uterine)	TM	TM
101809	4.5	M86849	"Homo sapiens connexin 26 (GJB2) mRNA, complete cds"	Other	Other
101478	4.5	M23379	RAS p21 protein activator (RTPase activating protein) 1	Other	Other
104695	4.5	AA012953	ESTs	TM	TM
100365	4.4	D78611	mesoderm specific transcript (mouse) homolog "EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence."	Other	Other
126819	4.3	AA305536	defensin; alpha 5; Paneth cell-specific	SS	SS
1011880	4.3	M97925	pigment epithelium-derived factor	Other	Other
126838	4.2	AA858097	cerebellar degeneration-related protein (62kD)	Other	Other
101684	4.2	M63256	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ	Other	Other
117634	4.2	N36421	WARNING ENTRY !!! [H.sapiens]	ESTs	ESTs
132109	4.1	AA599801	ESTs	Other	Other
115054	4.1	AA252863	ESTs	Other	Other
106553	4	AA454967	ESTs	Other	Other
119717	3.9	W69134	ESTs	Other	Other
131945	3.9	M87339	replication factor C (activator 1) 4 (37kD)	SS	SS
128790	3.9	AA291725	secreted frizzled-related protein 4	SS	SS
120562	3.8	AA280036	ESTs; Weakly similar to W01A6.c [C.elegans]	Other	Other
109517	3.7	D60799	ESTs		

FIG.-11Ab

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				SS	Other
102618	3.7	U65932 AA434441	extracellular matrix protein 1 frizzled (Drosophila) homolog 7	SS	Other
106286	3.7	D83004	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	SS	Other
133640	3.6		platelet-activating factor acetylhydrolase; isoform 1b; gamma subunit (29kD)		Other
100335	3.6	D63391			Other
104720	3.6	AA018441 U43701	ESTs ribosomal protein L23a	Other	Other
107348	3.6	AA236324	ESTs; Weakly similar to !!!! ALU CLASS A WARNING	SS	
134989	3.6		ENTRY !!!! [H.sapiens]		
111345	3.6	N89820 AA600147	ESTs; Weakly similar to Similar to NADH-cytochrome B5 reductase [C.elegans]	Other	Other
107053	3.6				
107240	3.5	D59368 AA620553	ESTs flap structure-specific endonuclease 1	Other	Other
107129	3.5	AA431505	Homo sapiens mRNA for putative Sqv-7-like protein; partial	TM	
134846	3.5	S58544	sperm associated antigen 1	Other	
101897	3.5	AA621169	ESTs	Other	
107151	3.5	AA411621	ESTs propionyl Coenzyme A carboxylase; alpha polypeptide	Other	
106012	3.4	S79219	ESTs	Other	
101950	3.4	H64938	ESTs	TM	
116844	3.4	AA937173 AA478587	ESTs leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL)	Other	
128025	3.4			Other	
106785	3.4			Other	
104518	3.4	R09815	ser-Thr protein kinase related to the myotonic dystrophy protein kinase		
117667	3.4	N39214			

**FIG.- 11Ac**

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE		ORF STRUCTURAL INFO
104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]		Other
105372	3.3	AA236481	ESTs	Other	
104896	3.3	AA054228	ESTs	Other	
113485	3.3	T87863	ESTs	Other	
127003	3.3	AA550806	ESTs; Weakly similar to (define not available 3882151) [H.sapiens]	TM	
100305	3.3	D50487	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)	SS	
134722	3.2	W47183	ESTs; Weakly similar to !!! ALU SUBFAMILY SB2 WARNING ENTRY !!! [H.sapiens]	Other	
126801	3.2	AA512902	ESTs	SS, TM	
133503	3.2	M33195	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	SS, TM	
132183	3.2	L19183	Human MAC30 mRNA; 3' end	TM	
105298	3.2	AA233459	ESTs	TM	
111046	3.2	N55514	ESTs; Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]	TM	
135309	3.2	D25984	ESTs	SS	
102808	3.2	U90426	nuclear RNA helicase; DECD variant of DEAD box family	Other	
100552	3.1	HG2167-HT2237	"Protein Kinase Ht31, Camp-Dependent"	Other	
127652	3.1	AA804487	ESTs	TM	
116127	3.1	AA459703	ESTs; Moderately similar to coded for by C. elegans cDNA CEESD64F [C.elegans]		
131904	3.1	AA143019	ESTs; Highly similar to surface 4 integral membrane protein [H.sapiens] transmembrane 4 superfamily member 3	TM	
126547	3.1	U47732	[H.sapiens] transmembrane 4 superfamily member 3	Other	
102823	3.1	U90914	carboxypeptidase D	SS	

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE		STRUCTURAL INFO
132298	3.1	N41849	Homo sapiens cytokine receptor related protein 4 (CYTOKR4) mRNA; complete cds		Other
127445	3.1	AA906286	ESTs		Other
134395	3.1	L09717	lysosomal-associated membrane protein 2 ESTs; Weakly similar to semaphorin C [M.musculus]		SS, TM
105743	3.1	AA293300			Other
125827	3.1	AI471525	YY1 transcription factor		Other
101229	3.1	L27943	cytidine deaminase		Other
102306	3	U33317	defensin; alpha 6; Paneth cell-specific "yc82f8.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:2242 5', mRNA sequence"		SS
107318	3	T74445			Other
120983	3	AA398209	EST		Other
134700	3	AA481414	golgi SNAP receptor complex member 1 ESTs		TM
131216	3	D31058			SS
127565	3	D79516	"HUM272B04B Human eiota polyA+ (TFUjiwara) Homo sapiens cDNA clone GEN-272B04 5', mRNA sequence."		Other
106882	2.9	AA489009	ESTs		Other
130874	2.9	T08287	ESTs		Other
101275	2.9	L37936	Ts translation elongation factor; mitochondrial ESTs		Other
111179	2.9	N67239			Other
126086	2.9	H70975	"yr73g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:210960 5', mRNA sequence."		Other
105365	2.9	AA236275	ESTs		Other
118789	2.9	N75416	ESTs		Other
115117	2.9	AA256492	H.sapiens PAP mRNA		Other
100484	2.9	HG1103-	"Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene Related"		Other
101300		HT1103			Other
		L40391	Homo sapiens (clone s153) mRNA fragment		

**FIG.- 11Ae**

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	Other
103075	2.9	X59543	ribonucleotide reductase M1 polypeptide		Other
132164	2.8	U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2		Other
106716	2.8	AA464962			Other
134098	2.8	X06323	Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3)	ESTs	Other
134485	2.8	X82153	cathepsin K (pancystolytic)	ESTs	SS
129634	2.8	AA150726			Other
112207	2.8	R49602		ESTs	Other
124904	2.8	R86970		ESTs	Other
125471	2.8	AA477571	UDP-glucose ceramide glucosyltransferase	ESTs	SS
132180	2.8	AA405569	fibroblast activation protein; alpha	ESTs	TM
104454	2.8	M84443	galactokinase 2	ESTs	Other
134282	2.8	T25508	neutrophil cytosolic factor 2 (65kD; chronic granulomatous	ESTs	Other
101558	2.8	M32011	disease; autosomal 2)	ESTs	Other
130529	2.8	AA173238	small inducible cytokine A5 (RANTES)	ESTs	Other
1011804	2.7	M86699	TTK protein kinase	ESTs	Other
109565	2.7	F01930		ESTs	Other
112427	2.7	R62604		ESTs	Other
115188	2.7	AA261819		ESTs	Other
121831	2.7	AA425374		ESTs	Other
132454	2.7	W78726	ESTs; Highly similar to serine/threonine kinase [H.sapiens]	ESTs	Other
116399	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene;	ESTs	Other
			complete cds	ESTs	Other
			Human mRNA for KIAA0202 gene; partial cds	ESTs	Other
100409	2.7	D86957		ESTs	SS, TM
130987	2.7	R45698		ESTs	
107217	2.7	D51095		ESTs	

**FIG.- 11Af**

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	STRUCTURAL INFO	
				ORF	SS
125698	2.6	AA748483	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds		SS
118722	2.6	N73563	"yf47c1.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:132 5', mRNA sequence"	Other	SS
104521	2.6	R11604	ESTs; Weakly similar to katanin p80 subunit [H.sapiens] protein tyrosine phosphatase type IVA; member 2 ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	TM	Other
130800	2.6	AA223386	Transcriptional Coactivator Pc4	Other	Other
134415	2.6	AA329274			
116461	2.6	AA621557			
100864	2.6	HG4297-HT4567	"zI43h5.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:54729 5', mRNA sequence"	Other	Other
103818	2.6	AA150614	ESTs	Other	Other
105713	2.6	AA291321	Human HF.12 gene mRNA	Other	Other
114969	2.6	AA250775	Human beige-like protein (EGL) mRNA; partial cds	Other	Other
130415	2.6	X07290	claudin 3	Other	Other
101791	2.6	M83822	ESTs	SS, TM	Other
128131	2.6	AI283162	Human mRNA for KIAA009.4 gene; partial cds	Other	Other
131564	2.6	AA491465	methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methenyltetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase	Other	Other
100279	2.6	D42084	ESTs	SS	Other
130149	2.6	J04031	ESTs	Other	Other
			Human mRNA for villin-		
119888	2.6	W81710			
126638	2.6	AA649257			
131672	2.6	X12901			

**FIG.- 11Ag**

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	ESTs
134405	2.6	J04177	collagen; type XI; alpha 1	Other	TM
101188	2.5	L20320	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	SS	SS
104534	2.5	R22303	ESTs; Weakly similar to putative p150 [H.sapiens]	Other	TM
135179	2.5	U43747	Friedreich ataxia	SS	SS
124308	2.5	H93575	ESTs	Other	TM
125621	2.5	A1051602	Coenzyme A acetyltransferase 2 (acetoacetyl acetyl-Coenzyme A thiolase)	SS, TM	Other
101342	2.5	L76191	interleukin-1 receptor-associated kinase 1	Other	Other
129351	2.5	AA167268	ESTs	Other	Other
103774	2.5	AA092898	ESTs; Weakly similar to R07G3.8 [C.elegans]	SS, TM	Other
131289	2.5	AA485697	ESTs	Other	Other
132094	2.5	W01996	ESTs; Highly similar to (define not available 4929683) [H.sapiens]	Other	Other
103223	2.5	X74801	chaperonin containing TCP1; subunit 3 (gamma)	Other	Other
105610	2.5	AA279991	ESTs	Other	Other
115719	2.5	AA416997	ESTs	Other	Other
134888	2.5	AA148094	Tat-interacting protein (30kL)	Other	Other
10564	2.5	AA262943	ESTs	Other	Other
129689	2.5	AA130156	ESTs	Other	Other
103391	2.5	X94453	pyrrole-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	SS, TM	Other
104182	2.5	AA479990	ESTs; Weakly similar to gltma amplified on chromosome 1 protein [H.sapiens]	Other	Other
123494	2.5	AA599786	ESTs	Other	Other
122905	2.5	AA470070	ESTs	Other	Other
109175	2.5	AA180496	ESTs	Other	Other

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				Other	Other
129907	2.5	D80170	ESTs	Other	Other
115142	2.4	AA258116	ESTs; Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	SS	Other
125474	2.4	AA151216	Homo sapiens 14-3-3 protein mRNA; complete cds	SS	Other
125745	2.4	AI283493	ribophorin II	Other	Other
100103	2.4	AF007875	dolichyl-phosphate mannose syltransferase polypeptide 1; catalytic subunit	Other	Other
102687	2.4	U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Other	Other
133170	2.4	U21049	epithelial protein up-regulated in carcinoma	SS, TM	Other
109141	2.4	AA176428	complete cds	Other	Other
132811	2.4	U25435	transcriptional repressor	SS, TM	Other
102862	2.4	X01057	interleukin 2 receptor; alpha	Other	Other
104300	2.4	D37933	syntaxis 1B	Other	Other
105091	2.4	AA148859	ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	TM	Other
110674	2.4	H89315	"yw25e09.s1 Morton Fetal Gochlea Homo sapiens cDNA clone IMAGE:253288 3', mRNA sequence."	Other	Other
122571	2.4	AA452600	EST	Other	Other
123421	2.4	AA598440	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	Other	Other
132181	2.4	AA046939	ESTs; Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]	SS	Other
129445	2.4	AA306121	ESTs; Moderately similar to FK506-binding protein 65kD	SS	Other
113923	2.4	W80763	[M.musculus]	Other	Other

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO		
				AA128100	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	Other
100598	2.4	HG2463-HT2559	Guanine Nucleotide-Binding Protein G25K			Other
130869	2.4	AA128100				Other
132393	2.4	W85888				Other
100830	2.4	HG4074-HT4344	Rad2			Other
133765	2.4	D21255	cadherin 11 (OB-cadherin; osteoblast)		SS, TM	
100867	2.4	HG4316-HT4586	Transketolase-Like Protein		Other	
119859	2.4	W80702			Other	
135269	2.4	M77698	YY1 transcription factor		Other	
115140	2.4	AA258030	ESTs; Weakly similar to (defline not available 3874821) [C.elegans]		Other	
102162	2.4	U18291	CDC16 (cell division cycle 16; <i>S. cerevisiae</i> ; homolog)		Other	
100372	2.4	D79997	KIAA0175 gene product		TM	
106981	2.4	AA521157	ESTs		Other	
130114	2.4	AA234717	ESTs		Other	
116129	2.3	AA459956	ESTs		Other	
122235	2.3	AA436475	ESTs		SS	
107315	2.3	T62771	Homo sapiens nucleoplasmn-3 (NPM3) mRNA; complete cds		Other	
125905	2.3	T69868	chaperonin containing TCF1; subunit 2 (beta)		SS	
133061	2.3	AB000584	prostate differentiation factor		Other	
107531	2.3	Y13936	protein phosphatase 1G (formerly 2C); magnesium-dependent; gamma isoform		Other	
125820	2.3	AA730136	teratocarcinoma-derived growth factor 1		Other	

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs;	Other
131725	2.3	AA456264	ESTs; Highly similar to (defline not available 4176448) [H.sapiens]	Other	Other
101228	2.3	L27706	chaperonin containing TCP1; subunit 6A (zeta 1)	Other	Other
132571	2.3	R84594	ESTs; Highly similar to (defline not available 4809026) [H.sapiens]	SS, TM	SS, TM
100090	2.3	AC002486	"Human BAC clone RG3;7O17 from 7p15-p21, complete sequence [Homo sapiens]"	Other	Other
103658	2.3	Z74615	collagen; type I; alpha 1	SS, TM	Other
104897	2.3	AA054641	ESTs	Other	Other
106818	2.3	AA480890	ESTs	SS	SS
113077	2.3	T40442	ESTs	SS	SS
128773	2.3	M28879	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)	SS	SS
129506	2.3	AA258286	Homo sapiens mRNA for KIAA0877 protein; partial cds	TM	Other
133746	2.3	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	Other	Other
134272	2.3	X76040	Lon protease-like protein	Other	Other
106267	2.3	AA431873	Homo sapiens clone 24711 mRNA sequence	Other	Other
133493	2.3	AA284143	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA; complete cds	Other	Other
104278	2.3	C02582	ESTs; Highly similar to (defline not available 5114045) [H.sapiens]	Other	Other
127211	2.3	AA480935	"aa28c03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564_5', mRNA/ sequence."	Other	Other
110721	2.3	H97678	ESTs	Other	Other
114774	2.3	AA150043	ESTs	TM	TM
132968	2.3	N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Other	Other
106916	2.3	AA490814	ESTs	Other	Other
113849	2.3	W60439	ESTs; Moderately similar to cbp146 [M.musculus]	Other	Other
131028		U20240	CCAAT/enhancer binding protein (C/EBP); gamma	Other	Other

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	STRUCTURAL INFO	
				SS	TM
130380	2.3	U55853	Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130)	SS	
			mRNA; complete cds	Other	
125390	2.3	H95094	KIAA0016 gene product	SS, TM	
127256	2.3	AA327550	ESTs; Weakly similar to !!! ALU SUBFAMILY SQ WARNING	Other	
			ENTRY !!! [H.sapiens]	Other	
132116	2.3	AA234767	ESTs	SS	
117765	2.3	N47797	ESTs	Other	
119126	2.3	R45175	ESTs	Other	
129482	2.2	AA435849	ESTs; Moderately similar to unknown protein [H.sapiens]	Other	
120493	2.2	AA255933	ESTs	SS	
108927	2.2	AA143493	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other	
122520	2.2	AA449427	ESTs; Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens]	Other	
125982	2.2	R98091	RAE1 (RNA export 1; S.pcmb) homolog	Other	
132325	2.2	N37065	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING	Other	
			ENTRY !!! [H.sapiens]	Other	
100287	2.2	D43950	Human mRNA for KIAA0038 gene; partial cds	Other	
114895	2.2	AA236177	Homo sapiens mRNA for KIAA0887 protein; partial cds	Other	
105038	2.2	AA130273	ESTs; Weakly similar to (defline not available 4240269) [H.sapiens]	Other	
105476	2.2	AA255473	ESTs	SS	
106942	2.2	AA496347	ESTs; Highly similar to gene 7442 protein [H.sapiens]	Other	
110566	2.2	H59990	ESTs	Other	
111068	2.2	N58397	"qn13h12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898183 3' similar to TR:O22813 O22813 PUTATIVE NAD (P)-DEPENDENT CHOLESTEROL DEHYDROGENASE."	Other	
127963	2.2	A1299013	; mRNA sequence."	TM	

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPI.ETE TITLE	STRUCTURAL INFO	
				ORF	INFO
130985	2.2	AA243700	ESTs	Other	
132877	2.2	R40685	Homo sapiens mRNA for KIAA0851 protein; complete cds	TM	
135242	2.2	M74093	cyclin E1	TM	
129468	2.2	J03040	secreted protein; acidic; cysteine-rich (osteonectin)	SS	
132616	2.2	AA386264	ESTs	SS, TM	
133780	2.2	M14219	decorin	Other	
121853	2.2	AA425887	ESTs	Other	
114608	2.2	AA079381	ESTs	Other	
129017	2.2	H13108	ESTs	SS	
132725	2.2	L41887	splicing factor; arginine/serine-rich 7 (35kD)	Other	
125606	2.2	R28463	ESTs	SS	
105538	2.2	AA258860	ESTs; Highly similar to (define not available 4583654) [H.sapiens]	Other	
133221	2.2	AA235289	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other	
106389	2.2	AA446949	ESTs	Other	
128949	2.2	AA190993	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Other	
120969	2.2	AA398116	ESTs	Other	
102495	2.2	U51240	Human mRNA for KIAA0085 gene; partial cds	TM	
101124	2.2	L10343	protease inhibitor 3; skin-derived (SKALP)	SS	
102778	2.2	U83463	syndecan binding protein (synterin)	Other	
107307	2.2	T52099	creatine kinase; mitochondrial 2 (sarcomeric)	Other	
111605	2.2	R11638	ESTs	Other	
101959	2.2	S80343	arginyl-tRNA synthetase	SS	
101031	2.2	J05070	matrix metalloproteinase 9 (gelatinase B; 92kD gelatinase; 92kD type IV collagenase)	Other	
131701	2.2	AA149008	ESTs; Weakly similar to III ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	TM	
105344	2.2	AA235303	ESTs		

**FIG.- 11 Am**

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTs	SS, TM Other
103166	2.2	X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Other	Other
131463	2.2	X74142	forkhead (Drosophila)-like 1	Other	Other
131412	2.2	U34044	Human selenium donor protein (selD) mRNA; complete cds	Other	Other
134982	2.2	N46086	ESTs	Other	Other
127236	2.1	AI341818	budding uninhibited by benzimidazoles 1 (yeast homolog)	Other	Other
104459	2.1	M91493	EST	Other	Other
124596	2.1	N70088	ESTs	Other	Other
105650	2.1	AA282347	ESTs; Highly similar to (disline not available 4454694) [H.sapiens]	SS	Other
134917	2.1	X87241	FAT tumor suppressor (Drosophila) homolog	SS	TM
1322478	2.1	H20906	Homo sapiens mRNA for KIAA0746 protein; partial cds	Other	Other
134464	2.1	N79354	ESTs; Weakly similar to Rga [D.melanogaster]	Other	Other
111221	2.1	N68869	ESTs	Other	Other
100892	2.1	HG4557-HT4962	"Small Nuclear Ribonucleoprotein U1, 1snrp"	Other	Other
117170	2.1	H98153	ESTs	Other	Other
124049	2.1	F10523	primase; polypeptide 2A (58kD)	TM	Other
131692	2.1	D50914	Human mRNA for KIAA0124 gene; partial cds	SS	Other
103003	2.1	X52003	trefoil factor 1 (breast cancer; estrogen-inducible sequence expressed in)	Other	Other
134085	2.1	U20979	chromatin assembly factor I (150 kDa)	Other	Other
126216	2.1	N23870	ESTs	Other	Other
102721	2.1	U79241	Human clone 23759 mRNA; partial cds	Other	Other
128040	2.1	AA918528	ESTs	SS	Other
101038	2.1	J05249	replication protein A2 (32kD)	Other	Other
106060	2.1	AA417287	C-terminal binding protein 2	Other	Other
103622	2.1	Z48042	basic transcription factor 3	Other	Other
127884	2.1	AA768630	ESTs	Other	Other

**FIG.-11An**

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE		STRUCTURAL INFO
			COMPILETE TITLE	ORF	
130911	2.1	W72906	HIRA interacting protein 4 (dnaj-like)	Other	
104260	2.1	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA; complete cds	Other	
120714	2.1	AA292689	ESTs	Other	
101578	2.1	M34423	galactosidase; beta 1	SS	
113443	2.1	T86158	Accession not listed in Genbank	SS	
101516	2.1	M28249	ESTs; Moderately similar to !!! ALU SUBFAMILY SB WARNING	Other	
106480	2.1	AA450373	ENTRY !!! [H.sapiens]	Other	
1111365	2.1	N92659	ESTs	Other	
121121	2.1	AA399371	ESTs; Weakly similar to (define not available 4688925) [H.sapiens]	Other	
124768	2.1	R40177	ESTs	Other	
102501	2.1	U51586	Human siah binding protein 1 (SiahBP1) mRNA; partial cds	Other	
106432	2.1	AA448850	ESTs	Other	
132812	2.1	R48108	accessory proteins BAP31/BAP29	Other	
125681	2.1	AA394176	cartilage oligomeric matrix protein	TM	
130511	2.1	L32137	ESTs	Other	
128219	2.1	AA978333	transmembrane 4 superfamily member 6	SS, TM	
130962	2.1	AA102051	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	TM	
101840	2.1	M93056	EST	Other	
123928	2.1	AA621363	ESTs; Moderately similar to !!! ALU SUBFAMILY SC WARNING	Other	
132073	2.1	N67408	ENTRY !!! [H.sapiens]	Other	
101671	2.1	M61832	S-adenosylhomocysteine hydrolase	Other	
107059	2.1	AA608545	ESTs	Other	
132791	2.1	AA446088	ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens]	Other	
103131	2.1	X65614	S100 calcium-binding protein P	Other	
104791	2.1	AA029046	ESTs	Other	

**FIG.-11AO**

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PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTS	Other
135181	2.1	AA621349	ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	ESTs	Other
104334	2.1	D82614	ESTs; poly(A)-binding protein-like 1	ESTs	Other
132103	2.1	AA025086	Human mRNA for KIAA026.1 gene; partial cds	ESTs	Other
126743	2.1	AA179253	ESTs; Moderately similar to similar to murine RNA-binding	ESTs	Other
100439	2.1	D87453	protein [H.sapiens]	ESTs	Other
114860	2.1	AA235112	ESTs; Weakly similar to !!! ALU SUBFAMILY J WARNING	ESTs	Other
116732	2.1	F13779	ENTRY !!! [H.sapiens]	ESTs	Other
131045	2.1	H30863	ESTs; Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canel protein. [H.sapiens]	ESTs	Other
133209	2.1	AA114183	ESTs; Moderately similar to glutamate pyruvate transaminase [H.sapiens]	ESTs	Other
101758	2.1	M77836	Human pyrroline 5-carboxylate reductase mRNA; complete cds	ESTs	Other
102214	2.1	U23752	SRY (sex-determining region Y)-box 11	ESTs	Other
130100	2.1	AA425593	Homo sapiens clone 669 unknown mRNA; complete sequence	ESTs	Other
109799	2.1	F10770	T-cell receptor; beta cluster	ESTs	Other
130860	2.1	U66061	Highly similar to 73 kDa subunit of cleavage and	ESTs	SS, TM
106685	2.1	AA461551	polyadenylation specificity factor [H.sapiens]	ESTs	TM
125724	2.1	AA083407	stimulated trans-acting factor (50 kDa)	ESTs	Other
134258	2.1	L28010	heterogeneous nuclear ribonucleoprotein F	ESTs	Other
129642	2.1	R50008	7-dehydrocholesterol reductase	ESTs	TM
125336	2.1	T86823		ESTs	Other
125303	2	Z39821		ESTs	Other

PRIMEKEY	FOLD UPREGULATED IN TUMORS	EXEMPLAR ACCESSION	COMPLETE TITLE	ORF STRUCTURAL INFO	
				ESTS	Other
100749	2	HG3521- HT3715	Ras-Related Protein Rap1 <sup>b</sup>	TM SS, TM Other	
126185	2	AI393989		ESTs	
126880	2	AI151406		ESTs	
105263	2	AA227926		ESTs	
123288	2	AA495836		EST ESTs	
105807	2	AA393803		ESTs	
105040	2	AA131047	KIAA0698 gene product	TM SS	
131977	2	F09788	procollagen-proline; 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase); alpha polyproline II	ESTs	
117992	2	N52000		SS, TM SS	
134037	2	X53586	Human mRNA for integrin alpha 6	Other	
132744	2	X54326	glutamyl-prolyl-tRNA synthetase	SS, TM SS	
101581	2	M34996	"Human MHC cell surface glycoprotein (HLA-DQA) mRNA, 3'end"	Other	
103576	2	Z26317	desmoglein 2	ESTs; Moderately similar to (define not available 4680395) [H.sapiens]	
131235	2	AA223284		ESTs; Weakly similar to sperm fertilization protein sp56 precursor [M.musculus]	
127910	2	AA781881		SS	
101552	2	M31642	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	Other	
106318	2	AA436570	Homo sapiens mRNA for pre-mRNA cleavage factor I subunit	Other	
101192	2	L20859	Human leukemia virus receptor 1 (GLVR-1) mRNA; complete cds	TM SS	
104592	2	R81003	Homo sapiens serine protease mRNA; complete cds	SS	
129095	2	L12350	thrombospondin 2	Other	
105705	2	AA290767	ESTs	SS, TM	
128461	2	M63262	arachidonate 5-lipoxygenase-activating protein		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENI: DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	ESTs
16074	>10	AA001507		other	other
25047	>10	AA011031		other	other
25082	>10	AA017257		other	other
16490	>10	AA026418		other	other
25179	>10	AA031268		other	other
25215	>10	AA035540		other	other
25282	>10	AA044825		other	other
16810	>10	AA053636		SS,	
16835	>10	AA054438		other	other
10747	>10	AA055841		other	other
10748	>10	AA055892		other	other
16993	>10	AA065300	Human mRNA	other	TM
17051	>10	AA070801		other	other
10840	>10	AA084104		other	other
7296	>10	AA085661		other	other
7325	>10	AA090842		other	other
17419	>10	AA113349	Weekly	?	?
17541	>10	AA127459		other	other
17559	>10	AA128407		other	other
25669	>10	AA128978		other	other
17600	>10	AA130596		TM	TM
10992	>10	AA132523		other	other
17654	>10	AA133250		EST	EST
17734	>10	AA137246		EST	EST
25801	>10	AA148530	- RC_AA	EST	EST
25806	>10	AA149007		?	?
11121	>10	AA156359	Human TAR D	?	?

FIG.-12Aa

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			EST's	EST's	
11160	>10	AA164289	EST's	EST's	other
25925	>10	AA164494	EST's	EST's	other
25934	>10	AA165355	Human clone	?	?
17987	>10	AA169379	EST's	EST's	other
18008	>10	AA171895	Homo sapiens	TM	TM
33953	>10	AA173290	Human HOXA	other	other
33980	>10	AA180223	CA_MP-DEPEN	other	other
34013	>10	AA190888	EST - RC_AA	other	other
34014	>10	AA191348	EST's	EST's	other
34015	>10	AA191353	EST's	EST's	TM
34070	>10	AA196549	EST's	EST's	other
18260	>10	AA206801	EST's	EST's	?
34105	>10	AA207123	EST's	EST's	SS,
34107	>10	AA209469	EST's	EST's	other
18330	>10	AA216722	Human mRNA	TM	other
18362	>10	AA223912	Ribonuclease	SS,	other
18392	>10	AA227751	EST's	EST's	TM
34188	>10	AA228030	EST's	EST's	?
34197	>10	AA232315	Homo sapiens	EST	?
25948	>10	AA234365	Homo sapiens	Evi-1	other
25951	>10	AA234556	EST	EST's	other
11561	>10	AA236533	EST's	EST's	other
26059	>10	AA236685	Human mRNA	EST's	other
26100	>10	AA242835	EST's Highly	EST's	other
11603	>10	AA243052	EST - AA2433	EST's	other
7785	>10	AA243375	EST's	EST's	?
34372	>10	AA251973	EST's	EST's	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	
26240	>10	AA252282	Human mRNA	TM	
34382	>10	AA252512	ESTs	other	
34391	>10	AA252703	EST - RC_AA	other	
26274	>10	AA253011	ESTs	?	
34400	>10	AA253400	ESTs	other	
26291	>10	AA253422	ESTs	?	
26355	>10	AA256379	ESTs	other	
11813	>10	AA258158	ESTs	other	
34518	>10	AA278721	ESTs	?	
26545	>10	AA278979	ESTs	other	
26574	>10	AA279504	ESTs	other	
34554	>10	AA280016	DNA polymerase	other	
34561	>10	AA280298	ESTs	TM	
26628	>10	AA280641	ESTs Highly	TM	
11969	>10	AA280670	ESTs	SS,	
34575	>10	AA280738	ESTs	TM	
26677	>10	AA281636	ESTs	?	
26700	>10	AA282197	EST	other	
34672	>10	AA284372	ESTs	other	
34692	>10	AA285079	ESTs	other	
12143	>10	AA290991	ESTs	other	
6092	>10	AA316272	EST	other	
34904	>10	AA321746	ESTs	other	
8111	>10	AA323787	ESTs	other	
8125	>10	AA330771	Human protein	TM	
26916	>10	AA331393	ESTs	other	
26926	>10	AA342402	ESTs	other	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ESTs	TM
26935	>10	AA347193	ESTs Weakly	TM	TM
35038	>10	AA350541	ESTs Modera	TM	TM
35049	>10	AA350857	ESTs	other	other
35106	>10	AA371561	EST Weakly s	?	?
35197	>10	AA398120	ESTs	other	other
35277	>10	AA398536	ESTs	other	other
35309	>10	AA398660	EST	other	other
35322	>10	AA398710	ESTs	TM	TM
27037	>10	AA400198	ESTs	?	?
35495	>10	AA400527	ESTs	other	other
27046	>10	AA400670	ESTs	other	other
35500	>10	AA400715	ESTs	other	other
12480	>10	AA403116	Homo sapiens	other	other
35693	>10	AA405485	ESTs Weakly	other	other
35697	>10	AA405512	ESTs	other	other
35766	>10	AA406169	Homo sapiens	other	other
35769	>10	AA406206	ESTs	other	other
35798	>10	AA410231	ESTs	other	other
35801	>10	AA410291	ESTs	other	other
35803	>10	AA410295	ESTs	TM	?
35822	>10	AA411144	EST	other	other
35874	>10	AA412024	ESTs	TM	?
35958	>10	AA412550	ESTs	other	other
36052	>10	AA417027	EST	other	other
36258	>10	AA423962	ESTs Weakly	other	other
36288	>10	AA424502	ESTs	?	?
36307	>10	AA424803	EST		

*FIG.\_ 12Ad*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	ESTs
36371	>10	AA426017	ESTs	TM	other
36395	>10	AA426353	ESTs	other	other
36405	>10	AA426406	Homo sapiens	other	other
36506	>10	AA429610	ESTs	SS,	other
36571	>10	AA430726	EST - RC_AA	?	other
36695	>10	AA433910	ESTs	?	?
36739	>10	AA435610	EST - RC_AA	?	other
36753	>10	AA435686	ESTs	?	?
36845	>10	AA436198	ESTs	SS, TM	?
36845	>10	AA436560	ESTs	SS,	?
13136	>10	AA436619	ESTs	other	?
13143	>10	AA442060	ESTs	?	?
36958	>10	AA442082	ESTs	?	?
36962	>10	AA442845	ESTs	?	?
36981	>10	AA443971	ESTs	?	?
13237	>10	AA445994	ESTs	?	?
13242	>10	AA446131	ESTs	?	?
37057	>10	AA446312	ESTs	?	?
37068	>10	AA446344	ESTs	?	?
37074	>10	AA446486	ESTs	?	?
37084	>10	AA447540	EST - RC_AA	?	?
37135	>10	AA447714	ESTs	?	?
37159	>10	AA447772	Homo sapiens	?	?
37168	>10	AA449311	ESTs	?	?
37246	>10	AA451707	ESTs	?	?
37310	>10	AA454610	ESTs	?	?
37453	>10	AA454632	ESTs	?	?
37456	>10			TM	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			ESTs	EST - RC_AA	
27787	>10	AA454660	ESTs	EST - RC_AA	?
37492	>10	AA455248	ESTs	EST - RC_AA	other
37546	>10	AA456641	ESTs	EST - RC_AA	TM
37601	>10	AA458864	ESTs	EST - RC_AA	other
37611	>10	AA458996	ESTs	EST - RC_AA	SS, TM
37615	>10	AA459101	ESTs	EST - RC_AA	other
37653	>10	AA460017	ESTs	EST - RC_AA	other
37677	>10	AA460530	ESTs	EST - RC_AA	other
37777	>10	AA464860	ESTs	EST - RC_AA	other
8648	>10	AA465016	ESTs	EST - RC_AA	?
37816	>10	AA469954	ESTs	EST - RC_AA	other
37829	>10	AA470084	ESTs	EST - RC_AA	other
28015	>10	AA477421	ESTs	EST - RC_AA	other
37978	>10	AA479294	ESTs	EST - RC_AA	other
37979	>10	AA479295	ESTs	EST - RC_AA	other
37983	>10	AA479348	ESTs	EST - RC_AA	other
14054	>10	AA485223	ESTs	EST - RC_AA	other
38121	>10	AA485724	ESTs	EST - RC_AA	other
28122	>10	AA485928	ESTs	EST - RC_AA	other
38167	>10	AA487207	ESTs	EST - RC_AA	other
38172	>10	AA487424	ESTs	EST - RC_AA	other
38179	>10	AA487492	ESTs	EST - RC_AA	other
38182	>10	AA487501	ESTs	EST - RC_AA	other
38194	>10	AA487969	ESTs	EST - RC_AA	?
28141	>10	AA488432	ESTs	EST - RC_AA	other
38211	>10	AA488687	ESTs	EST - RC_AA	other
38235	>10	AA489030	ESTs	EST - RC_AA	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
38280	>10	AA489791	EST - RC_AA	other
38316	>10	AA490500	Homo sapiens	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS,
38460	>10	AA504462	ESTs	other
38553	>10	AA521471	ESTs	other
38580	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA609177	ESTs	TM
38838	>10	AA609215	EST - RC_AA	?
38867	>10	AA609318	Human cbf-b m	TM
38871	>10	AA609333	EST	?
38970	>10	AA609749	ESTs	other
38984	>10	AA609839	ESTs Modera	?
39045	>10	AA610077	ESTs	?
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA	?
39110	>10	AA620709	ESTs Weakly	other
39176	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	ESTs	other
39232	>10	AA621409	ESTs	other
21	>10	AB000905	H sapiens hist	?
8963	>10	AFFX-HUMTF	AFFX-HUMTF	?
33890	>10	AFFX-HUMTF	AFFX-HUMTF	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR			ORF STRUCTURAL INFO
			ESTs	EST	ESTs	
39302	>10	C14944	other	?	?	
39329	>10	C20797	other	other	other	
28644	>10	D12163	other	other	other	
218	>10	D13540	PROTEIN-TYR	PROTEIN-TYR	PROTEIN-TYR	
236	>10	D13645	Human mRNA	Human mRNA	Human mRNA	
9127	>10	D30037	PHOSPHATID	PHOSPHATID	PHOSPHATID	
459	>10	D38293	Human mRNA	Human mRNA	Human mRNA	
39405	>10	D50975	TM	TM	TM	
39433	>10	D52037	other	other	other	
39436	>10	D52692	other	other	other	
39478	>10	D59388	TM	TM	TM	
39488	>10	D60831	EST	EST	EST	
39504	>10	D80632	ESTs	ESTs	ESTs	
765	>10	D86096	Prostaglandin	Prostaglandin	Prostaglandin	
787	>10	D86969	Human mRNA	Human mRNA	Human mRNA	
789	>10	D86971	Human mRNA	Human mRNA	Human mRNA	
39529	>10	F02202	ESTs	ESTs	ESTs	
39535	>10	F02450	ESTs Modera	ESTs Modera	ESTs Modera	
18676	>10	F04022	ESTs	ESTs	ESTs	
18718	>10	F04915	ESTs	ESTs	ESTs	
18762	>10	F09458	ESTs	ESTs	ESTs	
18782	>10	F09739	ESTs	ESTs	ESTs	
29080	>10	F13655	ESTs Modera	ESTs Modera	ESTs Modera	
19001	>10	H02890	ESTs	ESTs	ESTs	
19164	>10	H10395	ESTs	ESTs	ESTs	
39725	>10	H11323	ESTs	ESTs	ESTs	
19203	>10	H11593	ESTs	ESTs	ESTs	

*FIG.- 12Ah*

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO	ORF
			ESTs	ESTs		
19328	>10	H17808	ESTs	ESTs	?	
19387	>10	H20128	ESTs	ESTs	SS,	
39787	>10	H20131	ESTs	ESTs	?	
19389	>10	H20165	EST	EST - RC_H2	other	
39832	>10	H26279	ESTs	ESTs	other	
19591	>10	H40688	ESTs	ESTs	other	
29229	>10	H48459	ESTs	ESTs	other	
19727	>10	H52702	ESTs	ESTs	SS, TM	
19787	>10	H56679	ESTs	ESTs	TM	
39995	>10	H62474	EST	EST	?	
29331	>10	H68116	ESTs	ESTs	other	
29344	>10	H68839	EST	EST	other	
40064	>10	H72283	ESTs	ESTs	MITOCHOND	
40083	>10	H73466	ESTs	ESTs	TM	
19949	>10	H78263	ESTs	ESTs	other	
40204	>10	H88296	ESTs	EST - RC_H8	?	
29523	>10	H88353	ESTs	ESTs	Weakly	
29551	>10	H90134	ESTs	ESTs	?	
29645	>10	H95840	ESTs	ESTs	?	
20057	>10	H98079	ESTs	ESTs	other	
976	>10	HG2036-HT20	EST	EST - HG2036	?	
1158	>10	HG3344-HT35	EST	EST - HG3344	?	
1210	>10	HG37-HT37	EST	EST - HG37-H	?	
1346	>10	HG4716-HT51	EST	EST - HG4716	?	
1349	>10	HG4747-HT51	EST	EST - HG4747	?	
1445	>10	J03027	ESTs	MHC class I p	?	
1570	>10	K01383	EST	EST - K01383	?	

FIG.- 12Ai

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO
1684	>10	L07541	Replication fa	other
1852	>10	L17328	Human FEZ2	TM
1856	>10	L18920	MELANOMA-A	?
1863	>10	L19161	TRANSLATIO	other
2070	>10	L37378	Homo sapiens	SS,TM
2123	>10	L40396	Homo sapiens	other
2144	>10	L41349	Phospholipase	SS,
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other
2343	>10	M15353	Eukaryotic tra	TM
2627	>10	M29610	Glycophorin E	TM
2857	>10	M58597	Fucosyltransfe	TM
3021	>10	M68941	Protein tyrosin	other
3163	>10	M84424	Cathepsin E	?
3196	>10	M86917	Oxysterol bind	other
20088	>10	N20054	ESTs Weakly	other
29795	>10	N20641	ESTs Highly	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly	other
29893	>10	N23003	ESTs	TM
40498	>10	N26086	Homo sapiens	SS,
40559	>10	N33024	ESTs	SS,
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mR	other
20304	>10	N34686	Homo sapiens	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENIE DESCRIPTOR		STRUCTURAL INFO	ORF
40604	>10	N38893	Homo sapiens	other		
40631	>10	N45124	EST's	other		
40660	>10	N49104	NUCLEAR FA	other		
30610	>10	N50138	EST	?		
30617	>10	N50646	EST's	other		
30631	>10	N50807	EST	?		
30790	>10	N52935	EST	?	TM	
20564	>10	N55443	EST's	other		
40760	>10	N57927	EST's Weekly	other		
30938	>10	N58561	Cathepsin B	SS,		
20614	>10	N59230	EST's	other		
20657	>10	N62889	EST's	other	TM	
31136	>10	N63512	EST's Weekly	?		
40827	>10	N64051	Homo sapiens	other		
31310	>10	N66831	EST	?		
40876	>10	N67607	Human Rho-a	other		
20791	>10	N68057	Homo sapiens	other		
40905	>10	N68738	EST's	other		
40911	>10	N69114	H.sapiens mR	other		
40913	>10	N69218	EST's	other		
31484	>10	N69466	EST's	other	TM	
31619	>10	N73449	Homo sapiens	other		
41005	>10	N79516	EST	other		
31818	>10	N89774	EST's	other		
31872	>10	N91109	Homo sapiens	other		
41040	>10	N91948	EST's	other		
31944	>10	N93193	EST's	other		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			ESTs	ESTs	
41065	>10	N93618	ESTs	ESTs	other
32034	>10	N98926	ESTs	ESTs	other
41107	>10	R01634	ESTs	ESTs	other
41163	>10	R08176	ESTs	ESTs	other
21238	>10	R08564	Plasminogen-	ESTs	other
21240	>10	R08613	ESTs	ESTs	other
21412	>10	R20670	ESTs	ESTs	other
21519	>10	R27975	EST - RC_R2	?	?
41381	>10	R42278	H.sapiens mR	TM	?
32189	>10	R43183	ESTs	ESTs	?
32195	>10	R43471	ESTs Weakly	ESTs	?
21902	>10	R43822	EST	EST	?
21946	>10	R44707	ESTs	ESTs	?
22072	>10	R49406	ESTs	ESTs	?
32240	>10	R50976	Ribonuclease	ESTs	?
32258	>10	R55623	ESTs	ESTs	?
22258	>10	R56432	ESTs	ESTs	?
22282	>10	R59197	Human mRNA	ESTs	?
32277	>10	R61493	EST	ESTs	?
22372	>10	R62831	ESTs	ESTs	?
22400	>10	R64109	ESTs	ESTs	?
41593	>10	R64129	ESTs Highly	ESTs	?
10233	>10	R71427	THROMBOXA	ESTs	?
41654	>10	R76437	ESTs	ESTs	?
22557	>10	R76722	ESTs	ESTs	?
22576	>10	R79111	ESTs	ESTs	?
22593	>10	R79777	EST	EST	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				EST	EST - RC_R8
41678	>10	R80675		?	other
41719	>10	R89260		other	other
22793	>10	R96208		other	other
41752	>10	R97063		other	other
3375	>10	S50223		other	other
3406	>10	S66896		other	other
3522	>10	S80267		other	other
41793	>10	T03887		?	?
23198	>10	T40530		ESTs	Spleen tyrosin
23360	>10	T58531		ESTs	SQUAMOUS
32635	>10	T61116		ESTs	ESTs Weakly
42177	>10	T79786		ESTs	ESTs
23623	>10	T84047		ESTs	?
23662	>10	T86674		ESTs	?
42242	>10	T89579	Homo sapiens	ESTs	?
23759	>10	T90313		ESTs	?
23832	>10	T92018		ESTs	?
32740	>10	T92950		ESTs	?
42290	>10	T95105		ESTs	SS, TM
3598	>10	U01157		other	other
3659	>10	U04313		?	?
3799	>10	U10690		other	other
3870	>10	U14518		SS,	SS,
3913	>10	U16261		other	other
4029	>10	U21090		other	other
4157	>10	U28811		TM	TM
4178	>10	U30246			

FIG.- 12Am

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			+	-	
15006	>10	U30246	Human bumet	TM	
4193	>10	U31116	Human beta-s	TM	
4306	>10	U36798	Homo sapiens	TM	
4362	>10	U39817	Bloom syndro	other	
4386	>10	U40622	DNA repair pr	other	
4388	>10	U40714	Human tyrosy	other	
4455	>10	U43944	MALATE OXID	other	
4477	>10	U45880	Human IAP-lik	other	
4680	>10	U55766	Human Rev in		
4702	>10	U57341	EST - U57341	other	
4713	>10	U57721	Human L-kynu	other	
4787	>10	U61145	Human enhan	other	
4862	>10	U65437	Human homeo	?	
4945	>10	U69108	Homo sapiens	other	
4975	>10	U71088	Human MEK5	other	
4994	>10	U72514	Human C2f m	other	
5002	>10	U72761	Human karyop	other	
5021	>10	U73524	Human putativ	TM	
5149	>10	U79716	Human reelin	SS,	
5214	>10	U83303	H.sapiens mR	?	
5243	>10	U85946	Human brain s	other	
32789	>10	W02779	ESTs Modera	other	
42354	>10	W19346	ESTs	other	
42390	>10	W40150	Homo sapiens	other	
33006	>10	W46286	ESTs Weakly	TM	
33020	>10	W46891	ESTs Weakly	other	
33109	>10	W59961	Human mRNA	other	

FIG.- 12An

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	ESTs
24197	>10	W67277	ESTs	other	other
24215	>10	W69425	ESTs	other	other
33301	>10	W73883	ESTs	other	other
33343	>10	W79834	ESTs Weakly	other	other
33377	>10	W81219	ESTs Weakly	TM	TM
42602	>10	W86423	ESTs	other	other
33556	>10	W90705	Murine leukem	other	other
33616	>10	W93726	Protease inhib	TM	?
33666	>10	W95876	ESTs	SS,	SS,
5510	>10	X05360	Cell division c	TM	?
5558	>10	X07876	Wingless-type	SS,	?
5603	>10	X14253	Teratocarcino	SS,	?
5619	>10	X14850	HISTONE H2A	other	other
5623	>10	X14975	T-CELL SURF	SS,	?
5692	>10	X17644	G <sup>+</sup> to S phase	other	other
5789	>10	X54925	Matrix metallo	SS,	?
5799	>10	X55330	Aspartylglucos	TM	?
5802	>10	X55544	C <sup>y</sup> /CLIC-AMP	SS, TM	?
5857	>10	X58377	Human mRNA	other	other
5960	>10	X63575	A1Pase Ca++	TM	?
5963	>10	X63629	Cadherin 3 (P	other	other
5986	>10	X64810	Proprotein con	TM	?
6041	>10	X67155	MITOTIC KIN	other	other
6095	>10	X69962	Fragile X men	TM	other
6106	>10	X70683	SRY (sex dete	other	other
6155	>10	X74331	DNA primase	other	other
6167	>10	X74987	Ribonuclease	other	other

FIG.- 12AO

PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				TM	other
6188	>10	X76029	H.sapiens mR	TM	other
6315	>10	X81889	H.sapiens RB	TM	other
6382	>10	X85133	Human kinesi	?	other
6384	>10	X85137	UFIACIL-DNA	TM	?
6438	>10	X89398	H.sapiens mR	SS,TM	?
6449	>10	X89986	H.sapiens mR	TM	?
6478	>10	X91648	H.sapiens mR	?	?
6479	>10	X91653	EST - X91653	?	?
6494	>10	X92689	H.sapiens mR	?	?
6713	>10	Y08564	EST - Y08564	?	?
6790	>10	Y12394	Hcmo sapiens	?	?
24915	>10	YEL003w/	EST - YEL003	?	?
42773	>10	YEL019c/MMS	EST - YEL019	?	?
24545	>10	Z38462	ESTs	?	?
33713	>10	Z39427	ESTs	?	?
33791	>10	Z40883	ESTs	?	?
42766	>10	Z99394	ESTs Modera	?	?
21558	>10	R33112	Human AF-6 m	?	?
26718	>10	AA282576	ESTs	?	?
40113	9.9955090946	H78003	ESTs	?	?
10801	9.9879448276	AA069285	ESTs Weakly	?	?
37491	9.9513600842	AA455239	ESTs Highly	?	?
23900	9.9272347693	T95789	ESTs	?	?
254	9.9198395324	D14657	Human mRNA	?	?
6885	9.8970927914	Z29331	Ubiquitin-conj	?	?
29693	9.8850766398	H97819	ESTs	?	?
26482	9.8765189024	AA262491	ESTs	?	?

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FIG.- 12Ap

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				EST	ESTs
23123	9.8699502035	T25306	?	?	other
26525	9.8160399123	AA278392	Homo sapiens	EST	other
13110	9.7643356605	AA435840	Phosphoribos	EST	other
34863	9.7087597628	AA299784	ES Ts Weekly	EST	?
39432	9.7034550083	D51691	ES Ts	EST	?
31312	9.6513325388	N66845	ES Ts	EST	other
21112	9.6358446349	R01179	ES Ts	EST	?
31572	9.6254820695	N71294	ES Ts	EST	?
17903	9.6221229759	AA160259	ES Ts	EST	other
20747	9.6094813734	N66842	ES Ts	TM	other
4676	9.589223908	U55206	Homo sapiens	ESTs	other
34363	9.5627081023	AA251587	Homo sapiens	ESTs	other
39094	9.540768988	AA620636	Human beta-1	ESTs	?
3888	9.5372000133	U15128	ESTs	TM	other
39386	9.506250529	D12184	ESTs	ESTs	?
7674	9.4458059039	AA203742	Human DP pr	ESTs	TM
4192	9.4329744134	U31099	Human putativ	ESTs	TM
4507	9.422674945	U47050	ESTs Modera	ESTs	other
35606	9.412026255	AA402227	Human nuclea	ESTs	?
4970	9.3649551013	UT0862	EST	EST	?
19829	9.3432151573	H58813	ESTs	TM	other
14837	9.2878584141	T40145	ESTs	ESTs	other
17336	9.2822148675	AA099585	ESTs	ESTs	?
40541	9.2532836505	N30160	ESTs	EST	TM
29496	9.2487643833	H85434	ESTs	ESTs	other
29943	9.1797074262	N24786	ESTs Modera	ESTs	?
17997	9.1629681314	AA169633	EST	EST	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				EST's	EST's
21320	9.11243463318	R11673	EST's	other	other
13883	9.1178796537	AA476917	EST's Weakly	other	other
30539	9.08886887776	N49072	EST's	other	other
32778	9.0877919549	W02063	EST	?	?
26380	9.0809559378	AA257012	EST		
15888	9.0595893607	X95632	Hurnan Abl int	other	other
40812	9.0012874244	N63419	EST's	other	other
903	8.9640387908	D90070	ATL-derived P	TM	
22674	8.951577733	R87160	EST's	other	other
40807	8.9510132281	N62995	TRANSCRIPT	TM	
15244	8.9195644974	W00904	EST's	other	other
32296	8.8658776567	R67075	Zinc finger pro	other	other
18269	8.8575656769	AA209467	EST's	other	other
19662	8.8507626284	H47391	CLEAVAGE S	other	other
41607	8.833925517	R67868	Platelet factor	TM	
2548	8.8299864699	M25897	Hurnan tyrosy	other	other
7736	8.8279341243	AA232121	EST's	other	other
34490	8.7844537272	AA262354	EST's	other	other
38658	8.76669313482	AA599477	EST's	other	other
7528	8.765157554	AA149543	EST's	?	?
39939	8.7555031142	H53454	EST - RC_H5	other	other
25111	8.7232692309	AA020787	EST's	other	other
21655	8.716167279	R38239	EST's Highly	?	?
39663	8.665982852	H04756	EST - HG2510	other	other
1042	8.652112324	HG2510-HT26	EST's	other	other
32330	8.636115426	R77776	EST's	other	other
25382	8.6239456487	AA059007	EST's		

FIG.-12Ar

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				EST <sup>t</sup>	SS, other
27074	8.5900813076	AA401475	EST <sup>t</sup> Weakly MHC class II t	?	?
3955	8.5298909183	U18259	Human transp	?	?
4959	8.52646827	U70322	EST - M14123	?	?
2315	8.5259185808	M14123	EST <sup>t</sup>	?	?
37253	8.4896914632	AA449357	EST <sup>t</sup>	?	?
39624	8.471316877	F10836	EST <sup>t</sup>	?	?
23213	8.4569920887	T40891	TM	?	?
2798	8.455596435	M54995	Connective tis	?	?
41154	8.4413390141	R07499	EST <sup>t</sup>	other	other
32479	8.4093689549	T16282	EST <sup>t</sup>	other	other
41251	8.3587565415	R28279	EST <sup>t</sup>	other	other
19081	8.3583603183	H06701	EST <sup>t</sup>	other	other
21098	8.3105927559	R00545	EST <sup>t</sup>	other	other
14723	8.3061679053	D59894	EST <sup>t</sup>	other	other
37154	8.2994822341	AA447666	Human CENP	other	other
8068	8.2835586361	AA313387	EST <sup>t</sup> ; Highly	other	other
7485	8.281679348	AA129547	EST <sup>t</sup>	other	other
16501	8.2517969834	AA026969	EST <sup>t</sup>	other	other
34527	8.2419163754	AA279091	EST <sup>t</sup>	other	other
6700	8.1948675662	Y07867	H.sapiens mR	other	other
2852	8.1928816537	M58460	Human 75-kD	other	other
11188	8.1862492468	AA172372	EST <sup>t</sup>	other	other
42293	8.183311064	T95333	EST <sup>t</sup>	?	?
5443	8.1763317544	X02530	Interferon (gam	?	?
40937	8.1534810594	N70607	EST <sup>t</sup>	other	other
23371	8.1499496068	T59505	EST - RC_T59	?	?
26272	8.1339974519	AA252981	EST <sup>t</sup> ; Weakly	?	?

**FIG.- 12As**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
			ACCESSION	
17306	8.1332403762	AA086201	EST <sub>3</sub>	other
18497	8.1192326373	AA233795	EST <sub>3</sub>	other
235	8.0944363901	D13644	EST <sub>3</sub>	other
24525	8.0860187097	Z38347	TM	TM
7826	8.0750029554	AA248884	EST - AA2488	other
32142	8.0739258775	R38715	other	other
39067	8.0557768803	AA620405	TM	other
6235	8.0448957236	X78416	Castein alpha	other
29517	8.0017588725	H88261	EST <sub>3</sub>	other
28570	7.9852455973	C21104	Homo sapiens	other
39344	7.91162087762	C21034	EST <sub>3</sub>	other
18951	7.9002189759	H00580	EST <sub>3</sub>	other
18953	7.8709160227	H00615	EST <sub>3</sub>	other
18376	7.8564099916	AA226925	EST <sub>3</sub>	other
19830	7.84778447	H58911	EST <sub>3</sub>	other
36023	7.840835828	AA416881	EST <sub>3</sub>	other
13347	7.8344414518	AA449238	EST <sub>3</sub>	other
36614	7.8284591351	AA431466	EST <sub>3</sub>	other
2192	7.8254072032	L48211	Horro Sapien	?
33016	7.8006574068	W46577	H.sapiens mR	other
17215	7.7941954038	AA083044	EST <sub>3</sub>	other
34894	7.7659738105	AA311881	EST <sub>3</sub>	other
40614	7.695001222	N39257	EST <sub>3</sub>	other
36295	7.6834749899	AA424534	EST <sub>3</sub>	TM
19564	7.6744302788	H38833	EST <sub>3</sub>	SS,
16914	7.6686405336	AA058665	EST <sub>3</sub>	other
35967	7.6378079107	AA412694	Hurnan splicin	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	ESTs
21672	7.6364823402	R38635	ESTs	other	?
19918	7.6303275831	H69787	ESTs	other	?
10511	7.6297744492	AA024482	ESTs Highly	other	?
17721	7.6057911016	AA136590	ESTs	SS,	?
42302	7.6031859697	T96130	EST	other	other
26134	7.6000619383	AA243763	ESTs	other	other
18766	7.5621799008	F09497	ESTs	other	other
34492	7.501590494	AA262439	ATL-derived P	other	other
270	7.4512152125	D14822	EST - D14822	other	other
35975	7.4177746986	AA412738	ESTs	?	other
29842	7.4095809671	N21688	ESTs	other	other
35389	7.3913043319	AA399555	ESTs	other	other
19979	7.3868157166	H88477	C10C28 protein	other	other
5793	7.3865864025	X54942	EST - RC_H8	other	other
19978	7.380969715	H87770	EST - HG4126	?	?
1280	7.3691089318	HG4126-HT43	ESTs	other	other
31571	7.3676263454	N71250	ESTs Weakly	?	?
23765	7.3541191734	T90443	EST	?	?
35123	7.3397933455	AA380927	ESTs	other	other
38252	7.3341119467	AA489247	ESTs	other	other
38216	7.3282021037	AA488861	EST - RC_H7	?	?
29418	7.2489407005	H77915	Human mRNA	other	other
4834	7.1980951054	U63541	ESTs	TM	TM
42504	7.1913036522	W69803	H.sapiens mR	other	other
6111	7.158000198	X71125	ESTs Weakly	other	other
41773	7.154479618	T03024	ESTs	other	other
9951	7.1363626365	N71513	ESTs	other	other

FIG.-12AU

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			ESTs	EST - HG2160	
28109	7.0941968224	AA485212	other	?	
988	7.0783044659	HG2160-HT22	other	other	
29848	7.0610668511	N22107	other	other	
30628	7.0607950168	N50744	TM	TM	
22567	7.0225726353	R77771	TM	TM	
9347	7.0068323071	H03686	other	other	
11696	7.0026773299	AA252894	?	?	
40584	7.0010096333	N34870	EST	TM	
193	6.9767029188	D10923	ESTs	other	
18305	6.9740536051	AA214048	ESTs	other	
6078	6.9699682397	X69141	ESTs	other	
26741	6.902658703	AA283198	ESTs	other	
35069	6.89992865685	AA358397	ESTs	other	
23504	6.8977135983	T71042	ESTs	other	
299	6.8824513029	D16815	ESTs	other	
40583	6.8689903023	N34855	ESTs	other	
31428	6.8623762224	N68594	ESTs	other	
6169	6.8606959727	X75091	ESTs	other	
39524	6.8567355171	F01905	ESTs	other	
34578	6.8430689439	AA280837	ESTs	other	
38678	6.837527995	AA599920	ESTs	other	
23936	6.8251471804	T96930	Mish (Drosoph)	TM	
9326	6.8181321394	D89377	ESTs Highly	other	
19188	6.8067351968	H11255	Homo sapiens	other	
18185	6.7882148811	AA194983	ESTs Weakly	other	
27028	6.757529124	AA399630	EST	other	
41289	6.7519531681	R37265			

**FIG.- 12AV**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			EST - RC_AA	EST - J05614	
34511	6.7364448798	AA278298			other
1566	6.7056207716	J05614			?
25675	6.6692299748	AA129757			other
5814	6.6584342828	X56088	ESTs Highly CYTOCHROM	ESTs	SS, other
13861	6.6236291607	AA470145			other
29794	6.6026313352	N20598			other
39333	6.5902382643	C20910			other
3770	6.5835303599	U09609			?
31831	6.5829933764	N89894	ESTs		
33063	6.5808125026	W53000	Homo sapiens		other
20326	6.5640084836	N35583	ESTs Weakly		?
34384	6.5535703492	AA252537	ESTs		other
25599	6.5490481991	AA114091	ESTs		other
39749	6.5369363254	H14988	ESTs		?
42596	6.5200567072	W85900	ESTs		?
39606	6.5119482185	F10243	ESTs Weakly		?
14617	6.5105504748	C14983	ESTs		?
27831	6.45670814	AA456044	ESTs		?
34896	6.4496517783	AA312551	EST		?
27360	6.4434305006	AA425356	ESTs		TM
20126	6.4326610424	N22015	ESTs		TM
6663	6.4324809977	Y00291	RETINOIC AC	ESTs	other
30692	6.4196636207	N51563	EST		?
36472	6.4189542265	AA428633			other
9578	6.3961788753	H87652			other
39670	6.3818496159	H05626			other
22697	6.3652792447	R89218	ESTs		other

FIG.- 12AW

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				EST	TM
37308	6.3647804993	AA451694		EST	?
16101	6.3517262802	AA002147		EST	?
20629	6.3486854401	N59798		ESTs	other
36100	6.3364146287	AA417740		ESTs	?
15488	6.3252590241	W28097	Homo sapiens	ESTs	other
36667	6.3131273544	AA432136		ESTs	other
30766	6.3115037924	N52627		EST - RC_N5	?
32882	6.2745311453	W37683		ESTs	?
18072	6.2675797205	AA180448		EST	?
18231	6.2652604863	AA199747	Human mRNA	EST	other
38282	6.2514165678	AA489814		ESTs	?
28125	6.250317021	AA486073		ESTs	?
37464	6.2484456382	AA454747		ESTs	?
36618	6.1946328223	AA431478		ESTs	other
5082	6.1931116815	U78524	Human Gu bin	ESTs	other
1441	6.1777287039	J02963	Integrin alpha	ESTs	?
42105	6.14875944	T67710	SS,	ESTs	?
6061	6.1394863141	X68314	Glutathione pe	ESTs	?
32570	6.1156028796	T30222	Weakly	ESTs	?
32504	6.1019612076	T17063		EST	?
23335	6.0977927504	T56804		ESTs	other
10867	6.0970991075	AA088458		ESTs	?
30883	6.0911993489	N56923		ESTs	?
14528	6.0859008453	AA620295		EST	?
29454	6.0685955036	H81308	Homo sapiens	EST	?
6798	6.0539173278	Y13153		ESTs	?
21248	6.0525426545	R08871		ESTs	?

FIG.-12Ax

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	?
21940	6.0499964138	R44538	ESTs Homo sapiens	other	?
29066	6.0455247653	F10927	ESTs	?	SS,
18774	6.0446826953	F09609	ESTs	other	other
36722	6.0172343991	AA435512	ESTs Modera	other	other
18062	6.0034342969	AA179845	ESTs	?	?
22989	5.9992817406	T16305	ESTs	other	?
41745	5.9905623898	R95895	ESTs	other	?
8787	5.9894877658	AA504307	X-LINKED HE ESTs	other	?
20550	5.984861795	N55013	ESTs	other	?
26470	5.9417764101	AA262179	ESTs	other	?
16574	5.9356497569	AA031926	EST	other	?
693	5.9169537385	D80007	Human mRNA	other	?
4093	5.914830973	U25182	Human antiox	TM	?
1192	5.9086264407	HG3546-HT37	EST - HG3546	?	?
22956	5.8954735623	T10248	ESTs	other	?
36723	5.891606409	AA435524	EST	other	?
2114	5.8844986595	L40384	EST - L40384	other	?
26872	5.8688238789	AA291137	ESTs	other	?
6602	5.8663883018	X98266	EST - X98266	other	?
42701	5.8594493433	Z38612	ESTs	other	?
28573	5.84591116	C21118	ESTs	other	?
18290	5.8189427595	AA211901	Human mRNA	other	?
732	5.8043917941	D83781	EST - U91327	?	?
5330	5.8014145611	U91327	EST	?	?
33503	5.7990715189	W88720	Human platele	other	?
2553	5.7797505864	M26167	ESTs Weakly	other	?
34705	5.7658806254	AA286907			

FIG.- 12AY

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	
42665	5.7594091043	W93659	ESTs		other
38180	5.7539310793	AA487495	EST - RC_AA		other
4244	5.7476738809	U33286	Human chrom		other
32822	5.7418957453	W16834	ESTs		TM
3977	5.7245885557	U18991	Retinal pigment		?
24673	5.7202366155	Z39301	ESTs		TM
6928	5.7120261128	Z46629	SRY (sex-dete)		other
38726	5.7030796258	AA608733	ESTs		?
39290	5.6892372058	C14573	Human mRNA		other
11405	5.6818873796	AA232231	ESTs		other
22538	5.6792006591	R73567	Homio sapiens		TM
40747	5.6605393208	N56872	Homio sapiens		TM
31596	5.6554024604	N72094	ESTs		?
6329	5.6415652518	X82279	EST - X82279		other
31578	5.6273323661	N71361	ESTs		other
33207	5.6271818482	W70051	H.sapiens mR		other
2545	5.6105860146	M25753	Cyc in B1		other
22580	5.5988402647	R79156	ESTs		other
33592	5.5935314518	W93127	ESTs		other
28843	5.5734698755	D60252	CD(C21 HOMO		other
6160	5.5689050619	X74794	ESTs		other
37987	5.561345667	AA479666	Homio sapiens		other
42515	5.5217868611	W72116	Human hunting		other
4732	5.5130668527	U58522	Hydroxymethyl		?
3299	5.5099850678	M95623	ESTs		?
28320	5.473406981	AA599574	Human mRNA		TM
746	5.471260899	D84454			

FIG.- 12A2

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ORF	
39373	5.4635804954	C21517	ESTs	other	other
3117	5.4398413537	M81182	Peroxisomal m	other	other
21257	5.4343612441	R09196	ESTs Modera	other	other
31487	5.4318648859	N69507	ESTs	other	other
28954	5.4137130511	F03153	ESTs	other	other
38928	5.389782721	AA609595	ESTs	other	?
29903	5.3722320622	N23366	EST	TM	?
30925	5.3437432315	N58295	ESTs Weakly	TM	?
19091	5.3344615669	H07864	ESTs	other	other
28209	5.3138951918	AA491250	ESTs	other	other
9470	5.3118897984	H46617	EST - H46617	?	?
9435	5.3070056656	H30201	EST - H30201	other	other
28552	5.2954432572	C20914	ESTs	other	other
27411	5.2940164267	AA428137	ESTs	other	other
30615	5.2924125264	N50556	ESTs	TM	?
28313	5.2657977167	AA599309	ESTs	?	?
39321	5.2649035384	C20632	ESTs	other	other
29934	5.2531047395	N24194	ESTs	?	?
1094	5.2496703122	HG2846-HT29	EST - HG2846	TM	?
39578	5.2481126384	F08925	ESTs	other	other
11232	5.2466798424	AA186804	ESTs Weakly	?	?
2466	5.2426349328	M21539	Human small	other	other
26843	5.2387758661	AA287450	ESTs	?	?
40331	5.2353385567	H97562	ESTs Weakly	other	other
8035	5.205798365	AA305116	EST - AA3051	other	other
29793	5.1955425722	N20593	ESTs Weakly	?	?
34109	5.1481590107	AA210722	EST		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	Weakly ESTs
26408	5.14322577257	AA2558177		other	TM
19263	5.1427029807	H15054		other	other
24596	5.1416089352	Z38810		other	other
28589	5.1365059753	C21245		other	other
5684	5.1121931412	X17098		?	?
30710	5.1079347344	N51761		?	?
35765	5.0973514948	AA406167		?	?
26360	5.0863127861	AA256460		?	?
2351	5.0849612092	M15796	Proliferating c	other	other
30262	5.0836877534	N35065	Homo sapiens	?	?
41792	5.0737512465	T038886	ESTs	other	TM
36710	5.0703839864	AA434411	ESTs	?	?
39090	5.0546885407	AA620628	ESTs	other	other
42185	5.0539926381	T79951	ESTs	?	?
18745	5.0460321557	F09134	ESTs	other	other
35746	5.0396841996	AA406063	ESTs	?	?
35356	5.0354809581	AA399053	EST	?	?
36769	5.0312706878	AA435750	H.sapiens mR	other	other
36900	5.0279911548	AA436866	ESTs	TM	?
27595	5.0244757301	AA443328	ESTs	?	?
16290	5.0056611904	AA016145	ESTs	other	other
27117	5.0016146599	AA405098	ESTs	other	other
4304	4.9951954397	U36764	Eukaryotic tra	?	?
33458	4.9907402071	W86835	Homo sapiens	other	other
26693	4.980090679	A4282120	EST	?	?
12669	4.9758138651	AA417030	Homo sapiens	other	?
29701	4.9708526387	H97970	EST	?	?

FIG.- 12Bb

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	TM
20480	4.9557253636	N52168	EST - AA4812	other	
8720	4.9439110602	AA481218		SS, TM	
34828	4.9431269475	AA292436		?	
14985	4.941621032	U15128		?	
16115	4.9377553522	AA004420		other	
42506	4.9348587118	W70074		other	
34761	4.9316837445	AA287833		other	
11870	4.9281056201	AA262587		other	
23211	4.9258391854	T40889		other	
40611	4.9160502275	N39138		other	
42611	4.9128605354	W87006		other	
39652	4.9045174605	H03099		other	
17581	4.889674751	AA129395		?	
37239	4.8704375389	AA449121		?	
18712	4.8703618781	F04677		other	
30709	4.8611171953	N51752		other	
34179	4.8503613948	AA227903		other	
21433	4.825670988	R222183		?	
39731	4.8186142741	H11760		other	
31295	4.8116614607	N66653		other	
24647	4.804163055	Z39108		?	
31292	4.8008871817	N66615		?	
1285	4.7997542393	HG4157-HT44		?	
1106	4.7932425858	HG2981-HT31		other	
18212	4.7912262565	AA196506		other	
34367	4.782207045	AA251758		other	
34802	4.7797760205	AA291468		TM	

FIG.- 12BC

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ESTs	?
34762	4.7775301546	AA287834	ESTs	other	other
11595	4.7696612848	AA242819	ESTs	other	?
8295	4.7639839111	AA405082	ESTs	other	other
17622	4.758635576	AA131584	ESTs; Weakly	other	other
35781	4.7572463523	AA406335	ESTs;	other	other
34754	4.7483874972	AA287642	Human mRNA	?	?
23237	4.7444854356	T47291	EST	other	other
37667	4.7280445357	AA460318	ESTs; Highly	other	other
11568	4.7257189975	AA236786	ESTs;	other	?
38622	4.7190695733	AA598967	ESTs;	other	other
5137	4.7057359474	U79296	Dihydrolipoam	other	other
25038	4.7002244728	AA010065	CDC28 protein	other	other
19288	4.7000147312	H16567	ESTs;	other	other
32503	4.6979488292	T17045	Collagen type	TM	TM
3278	4.6953739298	M94055	SODIUM CHA	?	?
9696	4.6942061018	L38961	Integral transm	other	other
35400	4.6901390898	AA399591	Horro sapiens	other	other
35246	4.6862691303	AA398367	EST Weakly s	other	other
36387	4.6822499271	AA426270	ESTs;	other	other
21509	4.6730072542	R27314	ESTs	other	other
31381	4.6729672124	N67889	ESTs; Highly	other	other
26723	4.6727894925	AA282781	Human GAP S	other	other
36326	4.6703621086	AA425151	EST - RC_AA	other	other
17409	4.6688418667	AA113136	Human mitoge	other	other
4908	4.6552339935	U67156	ESTs	other	?
30594	4.6496238328	N49967	ESTs	other	?
38286	4.64639735	AA489847	ESTs Weakly	?	?

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	STRUCTURAL INFO	
				ESTs	other
13073	4.6426509459	AA433950	ESTs	other	other
40435	4.6240181066	N21614	Homo sapiens	other	other
14474	4.6228694379	AA609427	ESTs Modera	other	other
38213	4.615309907	AA488847	ESTs Weakly	?	?
5312	4.60644198	U90716	Human cell su	SS, TM	SS, TM
24225	4.6041550359	W70326	ESTs	?	?
35588	4.58689982366	AA401750	EST	?	?
29739	4.5863199051	H99626	EST	?	?
7203	4.5792992577	AA053096	EST - AA0530	SS, TM	SS, TM
2157	4.5772055869	L41939	Homo sapiens	?	?
32086	4.5661024279	R11510	ESTs	SS,	SS,
8085	4.5648114738	AA314779	ESTs Weakly	other	other
224	4.5622018989	D13633	Human mRNA	other	other
34006	4.5609980241	AA188761	DNA polymera	TM	TM
33656	4.5557384389	W95477	ESTs Weakly	other	other
34065	4.5537335124	AA195517	Aclenylsuccin	?	?
6028	4.5357922097	X66503	Cytochrome B	ESTs	ESTs
4166	4.5032930671	U29463	ESTs	SS,	SS,
40262	4.5024727522	H93562	ESTs	other	other
22687	4.5018672549	R88209	ESTs	?	?
41069	4.4977510482	N93969	ESTs	ESTs	ESTs
8264	4.4793100575	AA401334	ESTs	ESTs	ESTs
27588	4.472017297	AA443187	ESTs	ESTs	ESTs
35882	4.4717597552	AA412047	ESTs	ESTs	ESTs
34479	4.465519191	AA262080	Human bumet	TM	TM
15921	4.4548516436	Y12065	Homo sapiens	?	?
11279	4.4380038671	AA195399	ESTs	other	other

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	ESTs
39222	4.4367650786	AA621348	ESTs Highly	other	other
34428	4.4364736766	AA256526	ESTs	other	other
8771	4.432067373	AA491188	ESTs	other	other
22193	4.4189610024	R53891	ESTs	other	other
7898	4.4066170674	AA263032	ESTs	other	other
19902	4.3886145805	H66736	ESTs	other	other
9276	4.3868095209	D82374	ESTs	other	other
10716	4.3794529068	AA053319	ESTs	TM	TM
13193	4.3751913512	AA442763	ESTs	other	other
5690	4.3723059417	X17620	ESTs	other	other
35102	4.37147138	AA371509	EST - RC_AA	TM	TM
17983	4.3612985467	AA169226	ESTs	other	other
24962	4.3497206925	AFFX-HUMTF	ESTs	?	?
31680	4.3416539669	N74438	ESTs	other	other
27168	4.330306894	AA410258	ESTs	other	other
28731	4.3231846659	D20981	EST	?	?
28348	4.3212284906	AA608752	ESTs	other	other
16335	4.3019961487	AA018587	ESTs	?	?
33036	4.2915644973	W48580	ESTs	other	other
30180	4.2897721925	N33144	ESTs	SS,	SS,
35591	4.2895541242	AA401758	ESTs	?	?
25340	4.2721717135	AA054554	EST	other	other
28106	4.2659103748	AA485084	ESTs	other	other
38690	4.2649184307	AA600121	ESTs	other	other
20203	4.2626499431	N26855	ESTs	SS,	SS,
10251	4.2608760694	R76185	ESTs	SS,	SS,
12684	4.2604192389	AA417558	ESTs		

**FIG.- 12Bf**

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				TM	other
31636	4.2509469427	N73680	Natural resista	?	?
20769	4.2479765348	N67277	EST's	EST - K01884	?
1572	4.2353281083	K01884		other	other
10923	4.2292322072	AA116036		other	other
34380	4.2283792392	AA252414		other	other
10132	4.2222816115	R35733		other	other
16629	4.2161752119	AA036811	EST's	?	?
25146	4.1969683794	AA026356	EST's	ESTs Modera	ESTs
28730	4.1965943098	D20959	EST's	ESTs	ESTs
10200	4.1874912391	R64521	EST's	ESTs	ESTs
38695	4.1545794663	AA600176	EST's	ESTs	ESTs
31365	4.150549979	N67550	EST's	ESTs	ESTs
42379	4.1496120668	W37999	EST's	ESTs	ESTs
28050	4.1428703354	AA479139	Acid phosphat	?	?
2620	4.1386565707	M29474	Human recom	?	?
8927	4.1340593744	AF008442	Homo sapiens	?	?
13379	4.1269549188	AA449741	ESTs Weakly	?	?
5134	4.1218251808	U79293	Human clone	?	?
2626	4.1213948	M29581	Zinc finger pro	?	?
38005	4.1160483666	AA479969	ESTs	?	?
36575	4.1127196584	AA431085	ESTs Weakly	?	?
18296	4.1121837207	AA213620	EST - RC_H8	?	?
29531	4.1111459313	H88953	AFFX-HUMTF	?	?
143	4.1095880506	AFFX-HUMTF	ESTs	other	other
10970	4.0967613396	AA129390	Interferon (gam	SS,	SS,
25836	4.0952825397	AA152305	EST	?	?
19735	4.0937927853	H53038			

FIG.- 12B9

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	?
40711	4.0909709431	N53564	ES <i>t</i> s	other	
4149	4.0901471427	U28386	RA <sub>3</sub> (recomb	TM	
5767	4.0862784557	X53793	MULTIFUNCT	other	
5503	4.0861035825	X05232	Stromelysin	SS,	
20310	4.064111656	N34893	ESTs Highly	other	
456	4.0599824566	D38145	Prostaglandin	SS,	
7814	4.0559685576	AA248406	ESTs	other	
40230	4.0447282719	H90161	ESTs	SS,	
33651	4.039204804	W95409	ESTs	other	
16777	4.0231657929	AA046968	EST	?	
19110	4.0094905222	H08778	ESTs	other	
34442	4.0077010365	AA258093	HKR-T1	other	
5099	4.004992433	U79247	Human clone	TM	
8209	3.9990473163	AA384220	ESTs	other	
24408	3.9976586074	W90146	ESTs	other	
26596	3.9974919787	AA279943	Spleen focus	EST	
16485	3.9811264008	AA026269	ESTs	other	
32969	3.9804901745	W42451	ESTs Weakly	TM	
27006	3.9799768093	AA398695	EST	?	
29809	3.9526765967	N21043	ESTs	other	
9596	3.9440163451	H91564	Homo sapiens	other	
29024	3.9377933938	F09315	Homo sapiens	other	
21694	3.9356365584	R39317	Homo sapiens	other	
13207	3.929998104	AA443321	ESTs Highly	other	
37865	3.9143752629	AA476623	ESTs	?	
36201	3.9129828172	AA421164	AFFX-HUMTF	?	
8961	3.8981160269	AFFX-HUMTF			

FIG.-12Bh

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR	ORF STRUCTURAL INFO	
				ESTs	ESTs
17444	3.8927133917	AA115933		other	
25869	3.8919834527	AA157267		TM	
24862	3.89042252	Z41415		other	
26685	3.8889363206	AA281950		?	
42300	3.8850230366	T95850		?	
6495	3.8830844863	X92715	Zinc finger pro	other	
38604	3.8828045942	AA598803		TM	
36358	3.8826713718	AA425756		other	
30560	3.873276445	N49284		other	
14413	3.8724466158	AA600150		other	
23823	3.8574824967	T91805		other	
38158	3.853096838	AA487021	Homo sapiens	?	
2572	3.8519747554	M27281	EST	other	
40100	3.8464168967	H75933	Laminin recep	other	
40258	3.8462992993	H93340	ESTs	TM	
20944	3.8461621525	N74443		other	
20411	3.8459400966	N48963	Homo sapiens	other	
10345	3.8457714481	AA001663	ESTs	other	
31261	3.8451974374	N66248	EST	other	
8513	3.8378410994	AA446990	ESTs	other	
13877	3.8363409835	AA476604	ESTs	other	
40748	3.8253562321	N56879	EST	?	
14509	3.8152852193	AA609943	ESTs	other	
10281	3.8065567331	R80333	ESTs	other	
25284	3.8044158642	AA045074	ESTs	other	
6730	3.7900025129	Y09305	Y.sapiens mR	other	
16033	3.7884592402	AFFX-HUMIS	AFIX-X-HUMIS	?	

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		STRUCTURAL INFO
			FOLD	ORF	
39242	3.7827164808	AA621523	ESTs	?	
27354	3.7794760435	AA425221	ESTs	SS, TM	
4552	3.7777263605	U49188	Homo placen	other	
18385	3.7756199108	AA227219	Homo sapiens	other	
16754	3.76777416053	AA046067	EST - RC_AA	other	
12752	3.7671137403	AA421250	ESTs	other	
42463	3.7601033106	W60180	ESTs	?	
10614	3.7581669016	AA037357	ESTs	other	
867	3.7459337969	D87716	Human mRNA	other	
7608	3.7336047135	AA180967	ESTs	other	
31795	3.732738742	N80703	ESTs	other	
35377	3.7273784603	AA399453	EST - RC_AA	?	
22828	3.7243928524	R98192	ESTs	other	
25240	3.7243198336	AA039713	ESTs	other	
11008	3.7197361366	AA134289	ESTs Weakly	?	
4341	3.7162349944	U38545	Human ARF-a	other	
28833	3.7147818393	D59787	EST - RC_D5	SS,	
3750	3.7121007154	U09279	Collagen type	TM	
17483	3.6943413512	AA122147	ESTs	?	
16854	3.6915208471	AA055552	ESTs Weakly	TM	
3709	3.6891656771	U07550	Heat shock 10	other	
1608	3.6652978422	L00205	KERATIN TYP		
24577	3.6617721053	Z38727	Homo sapiens		
31032	3.6570916386	N62508	ESTs		
4951	3.6536195433	U69546	Human RNA b		
37660	3.6523275307	AA460225	ESTs		
20418	3.6495357091	N49209	ESTs		

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PRIMARY KEY	FOLD UPREGULATED OF TUMOR OVER NORMAL COLON	ACCESSION	UNIGENE DESCRIPTOR		ORF STRUCTURAL INFO
			?	?	
27995	3.6485167436	AA470155	Homo sapiens	EST's	other
7971	3.6434397185	AA287423	EST's	EST's	other
27606	3.64303453	AA443793	EST's	EST's	other
24677	3.6427250633	Z39338	EST's Highly	EST's	other
11070	3.6406198277	AA148521	EST's Weakly	EST's	TM
9328	3.6356048599	D89618	Homo sapiens	EST's	other
36826	3.634689802	AA435996	EST's	EST's	other
17678	3.6300045795	AA134275	Human HIV1 t	EST's	other
36209	3.6274694477	AA421266	EST's Weakly	EST's	?
34120	3.6258090412	AA211615	EST's	EST's	TM
38152	3.6246442011	AA486737	H.sapiens mR	EST's	TM
38463	3.6184693268	AA504491	EST's Weakly	EST's	TM
20064	3.6183699978	H98653	EST's	EST's	?
31256	3.5992620732	N66152	EST's	EST's	?
9713	3.5985228843	L44338	Homo sapiens	EST's	other
28622	3.5768056147	D11837	EST's	EST - RC_AA	?
38057	3.5736105703	AA481549	EST	EST - RC_AA	other
28763	3.5688723791	D45568	EST	EST - RC_AA	?
16996	3.5680705709	AA069038	EST's Modera	EST's	?
28628	3.5604144617	D11888	EST's	EST's	?
25804	3.5442954572	AA148885	Tumor protein	EST's	?
2492	3.5423964239	M22898	EST's Highly	EST's	other
14904	3.5411970737	T83389	H.sapiens RY	EST's	other
25265	3.5347588502	AA043765	EST's Weakly	EST's	other
13606	3.5327912417	AA456437	EST - RC_T96	EST - RC_T96	TM
42307	3.5318436465	T96595	TRANSCOBA	J05068	SS,
1544	3.526202414				

CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
CZA8	111929	3.7	R40057	prominin (mouse)-like 1
BCX2	128790	4.0	AA291725	secreted frizzled-related protein 4
CBC2	101809	5.7	M86849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBC1	100365	4.8	D78611	mesoderm specific transcript (mouse) homolog
CBC3	102618	2.5	U65932	extracellular matrix protein 1
	134804	6.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)
	104209	2.1	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated ESTs; Weakly similar to airway trypsin-like protease [H.sapiens]
CJA8	115697	8.1	AA411502	v-rat simian leukemia viral oncogene homolog A (ras related)
	124315	5.4	H94892	Homo sapiens CAGF9 mRNA; partial cds
	109415	4.3	AA227219	SRY (sex-determining region Y)-box 9 (campomelic dysplasia; autosomal sex-reversal)
	103613	5.1	Z46629	RAB6 interacting; kinesin-like (rabkin8in6)
	109166	6.2	AA179845	ESTs; Weakly similar to KIAA0226 [H.sapiens]
CJA9	116176	5.7	AA463725	ESTs
CGA7	115522	8.1	AA331393	ESTs; Weakly similar to unknown [H.sapiens]
	125852	5.7	H09290	ESTs
BCN5	112244	3.1	R51309	ESTs
CQA1	132592	5.6	AA129390	ESTs; Moderately similar to !!! ALU SUBFAMILY SC WARNING
BCN7	117280	5.4	N22107	ENTRY !!! [H.sapiens] karyopherin (impcritin) beta 2
	102663	4.8	U70322	ESTs
CQA2	104660	6.0	AA007160	ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING
	113702	2.4	T97307	ENTRY !!! [H.sapiens]
	100154	6.0	D14657	KIAA0101 gene product

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CODE	PRIMERKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
102260		3.7	U28386	Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds
101809		5.7	M86849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
133272		3.2	AA465016	ESTs; Highly similar to serine protease homolog
100365		4.8	D78611	mesoderm specific transcript (mouse) homolog
126819		4.7	AA305536	EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence.
132543		4.6	AA417152	ESTs; Highly similar to protein regulating cytokinesis 1 [H.sapiens]
103023		5.5	X53793	mulfifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase
132109		3.1	AA599801	ESTs
104037		3.5	AA372630	differentially expressed in hematopoietic lineages
104978		3.5	AA088458	ESTs; Weakly similar to !!! ALU SUBFAMILY J WARNING
				ENTRY !!! [H.sapiens]
108695		3.0	AA1121315	ESTs
107248		3.8	D59894	copine III
132902		3.4	AA490969	ESTs
120104		4.0	W95477	ESTs
128790		4.0	AA291725	secreted frizzled-related protein 4
101923		3.8	S75256	HNL=neutrophil lipocalin [human, ovarian cancer cell line OC6, mRNA Partial, 534 nt]
119943		3.4	W86835	ESTs
130648		3.9	AA075427	H4 histone family; member G
132358		3.5	X60486	frizzled (Drosophila) homolog 7
106286		3.2	AA434441	diubiquitin
117557		2.3	N33920	

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CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
129691	3.3	X06700	collagen; type III; $\alpha$ 1 (Ehlers-Danlos syndrome type IV; autosomal dominant)	
114767	4.5	AA148885	minichromosome maintenance deficient ( <i>S. cerevisiae</i> ) 4	
100335	3.8	D63391	platelet-activating factor acetylhydrolase; isoform 1b; gamma subunit (29kD)	
134989	3.5	AA236324	ESTs; Weakly similar to !!! ALU CLASS A WARNING ENTRY !!! [H.sapiens]	
110009	3.4	H10933	ESTs	
124059	4.0	F13673	ESTs; Weakly similar to epidermal type I keratin [H.sapiens]	
104755	2.2	AA024482	ESTs	
107151	3.4	AA621169	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens]	
132669	2.9	AA188378	ESTs; Weakly similar to 3NbHBst Homo sapiens cDNA clone yp19h1.r1 Soares breast 3NbHBst Homo sapiens cDNA clone	
104394	5.5	H46617	IMAGE:187921 5'; mRNA sequence	
117667	2.5	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase	
104954	3.3	AA074514	ESTs; Moderately similar to (defline not available 4753768) [H.sapiens]	
132994	3.7	AA505133	ESTs	
102681	3.7	U72761	karyopherin (importin) beta 3	
103989	2.2	AA314779	ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]	
132183	2.5	L19183	Human MAC30 mRNA; 3' end	
118695	3.0	N71781	ESTs	
100552	3.4	HG2167-	Protein Kinase H131, Camp-Dependent	
120471	2.5	HT22		
126547	4.2	AA251829	ESTs; Moderately similar to (defline not available 4680697) [H.sapiens]	
106057	3.3	U47732	transmembrane 4 superfamily member 3	
		AA417067	ESTs	

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CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
125103		4.0	T95333	ESTs; Weakly similar to Strabismus [D.melanogaster]
135243		3.4	AA215333	ESTs
121457		2.5	AA411448	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
131216		2.7	D31058	ESTs
112971		2.4	T17185	ESTs
111179		2.1	N67239	ESTs; Moderately similar to !!! ALU SUBFAMILY SC WARNING
123533		2.3	AA608751	ENTRY !!! [H.sapiens]
105175		2.4	AA186804	ESTs; Weakly similar to unknown [S.cerevisiae]
105156		2.7	AA172372	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING
111223		2.5	N68921	ESTs; Weakly similar to neogenin [H.sapiens]
132180		2.7	AA405569	ESTs; fibroblast activation protein; alpha
106400		2.1	AA447621	ESTs
129260		3.1	AA093834	ESTs; Highly similar to (defline not available 4679014) [H.sapiens]
115291		3.9	AA279943	ESTs; Weakly similar to Yel007c-ap [S.cerevisiae]
128628		2.1	C14037	ESTs; Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds
116399		2.7	AA599729	Homo sapiens
130987		3.5	R45698	ESTs
105082		2.6	AA143763	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]
103453		3.2	X99585	H.sapiens mRNA for SMT3B protein
115947		2.6	AA443793	ESTs
105012		2.8	AA116036	ESTs; Highly similar to (defline not available 4589929) [H.sapiens]
105507		3.2	AA256678	ESTs; Moderately similar to (defline not available 4106061) [H.sapiens]
130800		2.6	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]

**FIG.- 13Ad**

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CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
116461		3.4	AA621557	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sap ens]
129945		2.5	AA232104	ESTs; Highly similar to (define not available 4929579) [H.sapiens]
100864		2.1	HG4297- HT45	Transcriptional C-activator Pc4
128131		2.3	AI283162	claudin 3
131564		2.8	AA491465	ESTs
100279		3.1	D42084	Human mRNA for KIAA0094 gene; partial cds
134405		1.8	J04177	collagen; type XI; alpha 1
130287		2.6	AA113149	tumor suppressor; subtransferable candidate 3
108828		2.1	AA131584	ESTs; Weakly similar to coded for by C. elegans cDNA crn16f6 [C.elegans]
131289		2.2	AA485697	ESTs
109141		4.2	AA176428	ESTs
119307		2.5	T32108	ESTs
134319		2.1	AA129547	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
133458		5.0	M18728	non-specific cross-reacting antigen
116732		2.3	F13779	ESTs; Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
CGA8	115239	3.0	AA278650	ESTs

*F/G.-13Ae*

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CODE	PRIMEKEY	D OF TUMOR OVE	EXEMPLAR ACCESSION	COMPLETE TITLE
CZA8	111929	3.7	R40057	prominin (mouse)-like 1
BCX2	128790	4.0	AA291725	secreted frizzled-related protein 4
CBC2	101809	5.7	M86849	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBC1	100365	4.8	D78611	mesoderm specific transcript (mouse) homolog
CBC3	102618	2.5	U65932	extracellular matrix protein 1
CJA8	115697	8.1	AA411502	ESTs; Weakly similar to airway trypsin-like protease [H.sapiens]
CJA9	116176	5.7	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]
CGA7	115522	8.1	AA331393	ESTs
BCN5	112244	3.1	R51309	ESTs (now Sulfatase by in-house sequencing)
CQA1	132592	5.6	AA129390	ESTs
BCN7	117280	5.4	N22107	ESTs; Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTR Y !!! [H.sapiens]
CQA2	104660	6.0	AA007160	ESTs

*FIG.-14*

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ATGACCATGATAAGGCCAAGCTTGGCACGGAGAACGGCCACTTGGCCCTTGTCACCAAAACAAAGGAGAACGGTGCAGAGC  
TGTCCCGTGTGGACCCCTGACTCACCCGAATCATTCAGAGATAAAAATAI GTAAATCCCCTGACTCAATTCCAGAATCATGAAA  
AGCAGGAAAGCAGGATCTCAGGGCTACTGCAAAAGTTCCCTCACCCTGACCCAGAACGCTGAGAAGCTGAGAATGCTGTGTT  
TCCTCAGGTAACAGAGATTCAAGGGTACCTTCAGAAGGAAAGGAATCTCCTACAGAGATGAGTGCATCCAAACCTGGAAA  
AAATAAAAAGAACACTGCAATTCACTACTCCAAACTTTAAGGAAGCTTCATGAACTTAAAGGAAATATGCAATTAAAGGGAA  
AATATATTGAGAGAAAAGAACATTGAGAAACACAATTTCATGAAAGAACATTTGAGAAAGATAATGAGCATAAAGGAAACAA  
GGGCTCAGGACTCCAGTACCTCCAAGAGGGAAAGACTCTCTGTGGCTTCTGAAGGGGTCTGCTATCTCTGAGCTAAACCG  
GTCTGTGGCCCTGCAAGTCAGAGTACCTTGGGTCTGCTGAAGGGGTCACTCTAGGCTCTGCTATCTCTGAGCTAAACCG  
GTGTCAAGGTTTCAGCTGCTACTAAAGATAATGAGCATAAAGGCTTCACTTACCAAAAGACTCCAGGAGAACCTCCAGAA  
GTGACCGGTGTCTGGGGCACCCAAAAGGGCAGGGCTGTGCTTGGACACACAAATTAAGGACCATCAGGGGAAATTCCTG  
TGCTGTTATTACCCCATTCAGTGACAACACTGAGGCAACGGCAGACTCCAACTCTGGGCAATCTAAAGGAAACCGTCT  
AAGCAAGTTGTCTCGTCCCCTCAACTATGAAACCACAAAGGAAAGCTAAACCCATCTCCAGACAAAGGAAGAGCA  
TATCTAAATCAACATGTCAACAGAATTAAACTCTAACAGAAACTTCAACTTCTGATTTCACCTTGTAAATTTTTTTGTGTT  
ACGGAGAAACGGGAGCAAGAACGAAAGGAGAAGCAAGGAAAGCTTGTGTTACTTAAAGTGGATGGTTTCACTGTTCT  
ATCTCTGAAAGACGTTATCACCTTAAGCTCAAACTCTGGATGGTTTCAACTTGTGTTCTAGATTAAATCTGTT  
CTAACCGAGACCCATCCTAAAAATTCTGTTACTTACCTAGGTGAATTTGTTCTAGATTAAATCTGTT  
ACAGAACTGCAAGTCTGCTAGGAGATCTTCTGCTAAAGGCCACCTCTCACTCTGTTTAAAGCTTACCTTGTGTT  
TAACAGAAATAGGGTAAAGCTGGGATAGAAAGGCCACCTCTCACTCTGTTTAAAGCTTAAAGCTTACCTTGTGTT  
CATATACTGTTGGTTATGACATCAATATTACCTAGGTGAATTTGTTCTAGATTAAATCTGTT  
ACAGAACTGCAAGTCTGCTAGGAGATCTTCTGCTAAAGGCCACCTCTCACTCTGTTTAAAGCTTACCTTGTGTT  
TAACAGAAATAGGGTAAAGCTGGGATAGAAAGGCCACCTCTCACTCTGTTTAAAGCTTACCTTGTGTT  
CATATACTGTTGGTTATGACATCAATATTACCTAGGTGAATTTGTTCTAGATTAAATCTGTT  
GTAATTGGCCATCTGTCACTCACTTAACTCACAATTTGCTTAAATGCTTAAAGACAGGGTCTCA  
ATAGCCCTATGAAATGGCAGGGATTAACTGGCTTCACTGTTCTGCTTAAAGCTTACCTTGTGTT  
AACTCCACCAAAATGTAATGTTTATGTCATGTTTCAAAATTTCTCATTTCTCATTTCTCATTTCTCATTTCTCATTTCT  
TCAGTGGAGCTTCTGACTTCTGACTTTATACTGCTCAAGATGGTCAAAAAAA

FIG. - 15

ATGCCATTACGCCAAGCTTGGCACGGGACAGCCACTTGGCCA'TGTACCAAAACAAGGAGAACGGTGCAGAAC  
 TGTCCGTGTGGACCCCTGACTCACCGAGATCATTCAGAGATAAAATAAATTAAGTTAACTCCACTGAAATTCCAGAATCATGAA  
 AGCAGGAAGGCCAGGATCTCAGAGCTACTGCCAAAGTCCCTCTCCACCA'GAGGACCCAGAACCTGAGAAATGCTGT  
 TCCTCAGGTAAACAGGATTCAAGGTACTTCAGAAGGAAGAAATCTCTCACACAGATGAGTCATCCAAACCTGGAA  
 AAATAAAAGAAACTGCAATCAACTACTCCAACATTAAAGGTTCAAGGAAACACAATTCCATGAATGAACCTGAAGGAGG  
 AATATAATTGAGAGAAAAGAACATTITGAAGAACACAATTCCATCAACTGAGCTCTGGCTTCTACTCCACAGC  
 GGGTCAGGCACTCCAGTACCTCCAGGAAAGACTCTGTGGCTGACTCAAGGGCTCAACTCAAGGCTCTGCT  
 GTCTTGCGCCCTGCAAGTCAGAGTACCTTGCGTCAACTAAAGATAATGAGCATAAGCGTTCACTGACC  
 GTGTCAGGGTCTGGGGCACCCAAAGGGGACCCAAAGGGGACCCAAAGGGGAGGGTGTGCT  
 GTGACCCGTGTCTGGGGCACCAAAAGGGGACCCAAAGGGGAGGGTGTGCT  
 TGGTGTATTACCCATTCAAGTTGACAACCTGAGGGCAAGCAGACTCAGTC  
 AAGCAAGTTGTCTCGTCCCCCTCAACTATGAACCCACAAAGGAAGCTAAACCC  
 TATCTAAATCAACATGTCAACAGAAATTAAACTTCTACAAGAAACTTAC  
 ACGGAAAGAACGGCAGGAAGAACGAAAGGAGAACGAAAGGAGAAC  
 AT[REDACTED]

FIG.- 16

MTMITPSLARGRQPLGHVTKTRRRCKTVRVDPDSQQNHSEI[KISNPTEF[NHIEKQESQDILRATAKVPSPPD  
 ESGNRDSKVPSSEGKKSLYTDDESSKGKMKRTAITPNFRKLHEAHFREMEISIDQYIERK[KHFEHNISMNELKQQPI  
 NGGVRTPVPPRGRLSVASTPISQRRSQGRSCGPASQSTLGLKGSILKRSALISIAKTVRFSALT  
 VTVSGGTOKGEAVLGTHKLKTITGNSAAVITPFKITTEATQTPVSNKPKVFDLKASLSRP  
 YEPHKGGKLKPWQSKENN  
 YLNQHVNRIIFYKTYKOPHLQTKEEQRKKREQERKEKAKVLGMRRGLJIAED

FIG.- 17

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Amino-CKVLG MRRGL IIAED-COOH**FIG.\_18**Acetyl-KQPHL QTKEE QRKKC-Amide**FIG.\_19**

<b>human_CAA2</b>	-----KKHFEHHSMNEIKQPIINKGGVVRTPVPPGRLLSVASTPISQRSS
<b>mouse_CAA2</b>	ARFKRMEISIDEYIMRKKHKLKEHSSLNEIKLDICK--GIVTPVPPGRLLSVPCTPARQQCP
	*** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :
<b>human_CAA2</b>	QGRSCGPASQSTLGLKGSLKRSAlISAATKGVRI"SAATKDNEHRSLSLTKPARKSAHVTVS
<b>mouse_CAA2</b>	QG-----H-S-ATKMNVR"SAATKDNEHKCSLTCKTPARKSPHVTAP
	** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :
<b>human_CAA2</b>	GGTQKGEAVLGLTHKLKTITGNNSAATVITPFKLTTATQTPVSNKKPVFDLKASLSRPLNYE
<b>mouse_CAA2</b>	GSASKGQAVFRTPKSKATERTSIAVITPFKLMTATQTPSSSSKPKVFDLKASLSRPLNYK
	* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :
<b>human_CAA2</b>	PHKGKLKPWQSKENNTLNQHVNRLNFYKKTQKOPHLQTKEEQRKREQERKEKKAKVLG
<b>mouse_CAA2</b>	PHKGKLKPWQAKENNSLNERVSRTFHRTKTYKOPHLQTREERWKRQEQRKEKEKILLE
	***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :
<b>human_CAA2</b>	MRRGLIJAED-
<b>mouse_CAA2</b>	ARRNLGVTKAQ
	** : * : :

**FIG.\_20**

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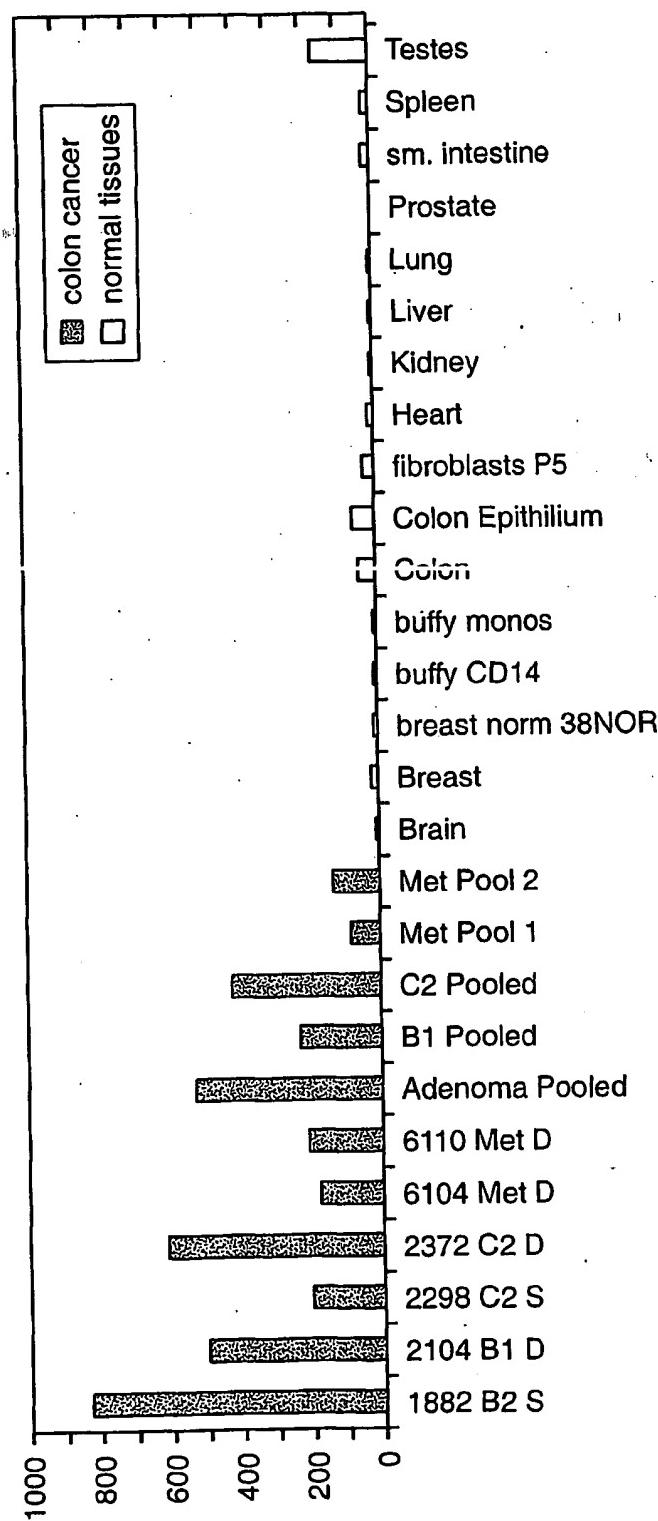


FIG. 21

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**FIG.-22A**

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FIG.\_22B

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**FIG. 23A**

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FIG.-23B

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MEPRTAPSGAPGLAGVGETPSAALAARVELPGTAVPSVPEDAAPASRDGGGVRDEGPAAAGDGTGRPLGPTPSQR  
 FQVDLVSENAGRAAAAAAAAAAAAAAAAGAGAGAKQTPADGEASESEPAK3SEEAKGRFRVNEDPAASSSAEDSLSDAA  
 GVGVDGPNVSFONGGDTVLSEGSSLIHSGGGGSGSHHQHYYDDTHNTTYLRLTGFHNTMDAVERDHYRHTAAQLGEKLLR  
 PSLAELHDELEKEPFEDGFANCEESTPTDRAFTAVVTTAeskGVVKFGWIKGVLRVCMLNIMGVILFIRLSWIVGQAGIGLS  
 VLVIMMATVTTITGLSTSALATNGFVRGGAYYLISRSLGPEFGGAIGLIFAFANAVAVAMVVVGAETVVELLKEHISI  
 LMIDEINDIRIGAITVILLGIVSAGMEEWAKAQIVLVLVLLLAIGDFVIGTFIPLESKPKGFFGYKSELFNENFGPD  
 FREEETEFSVFAIFFPAATGLAGANISGDLADPQSAIPKGTLAILITLIVYGLIAVSVGSCVVRDATGNNNDTIVTEL  
 TNCTSAACKLNFDFSCCESSPSCSYGLMMNFQVMMSVSGFTPLISAGIFSATLSSALASLVSAPK1FFQALCKDNITYPAFMQ  
 FAKGQGKMNNEPLRGYIILTEFLIALGFIL  
ILCCIVMFEVINWWAALTYVIVLGLYTIVTYKKPDVNWGSSSTQALTYINLQHSIRLSGVEDHVKNFRPQCLVWTGAPNS  
 RPALLHLVHDFTKVNGLMICGHVIMGPRROAMKEMSIDQAKYQRWLKNUMKAFYAPVHADDLREGAQYIMQAAGLGRMK  
 PNTLNLVGEFKKDWLQADMRDVDWYIINLFHDAFDIQQYGVVVIRLKEGLDIISLQGQEELLSSQEKSPTKDVVVSVEYSKKS  
 DLDTSKPLSEKPITHKVEEDEGKTAQPPLKKESKGPIVPLINVAQOKLLEASTFOQKKQGKNTIDVWWLFDGGTLILLIP  
 YLTITKKKKMKDCCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLCINTKPKKENNIAFEETIEPYRIHEDDKEQ  
 DIADKMKDEPWRITDNELEYKTKTYQRIRLNEILKEHSTANTIVMSIPVARKGAVSSALYMAWLEALSKDLPPILLV  
 RGNHQSVLTFYS

FIG.-24

Peptide Names	Solubility	
CAA9p1	1mg / 1ml H <sub>2</sub> O	H-CDPAASSSAEDSLS-D-NH2
CAA9p2	1mg / 1ml H <sub>2</sub> O	Ac-KKSDLDTSRPLSEK-C-NH2
CAA9p3	1mg / 1ml H <sub>2</sub> O	Ac-PLLKRESKGPIVPLC-NH2
CAA9p4	min.amt.DMSO / H <sub>2</sub> O	Ac-EHSILMIDEIC-NH2
CAA9p4MAPS	1mg / ml buffer pH7.5	Ac-EHSILMIDEIC-on 8-Branch Maps
CAA9p5	1mg / 1ml H <sub>2</sub> O	Ac-DFREEETC-NH2
CAA9p5MAPS	1mg / 1ml H <sub>2</sub> O	Ac-DFREEETC-on 8-Branch Maps

FIG.-25

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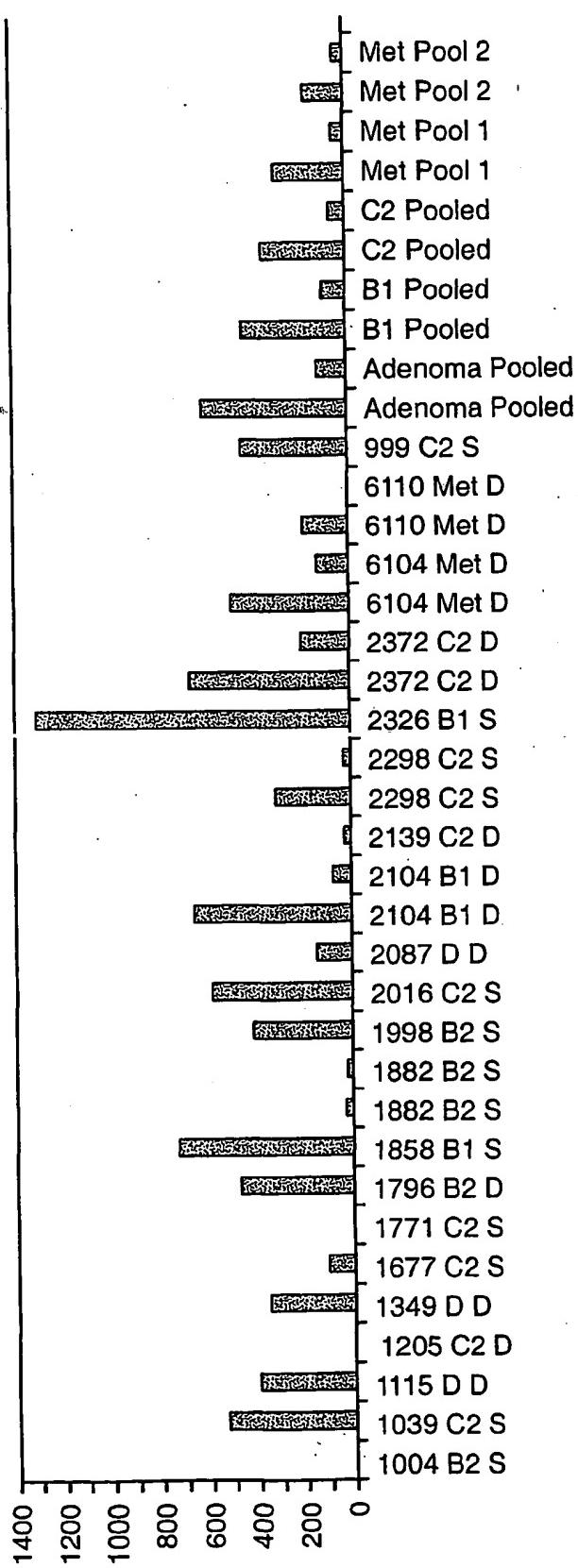


FIG.\_26A

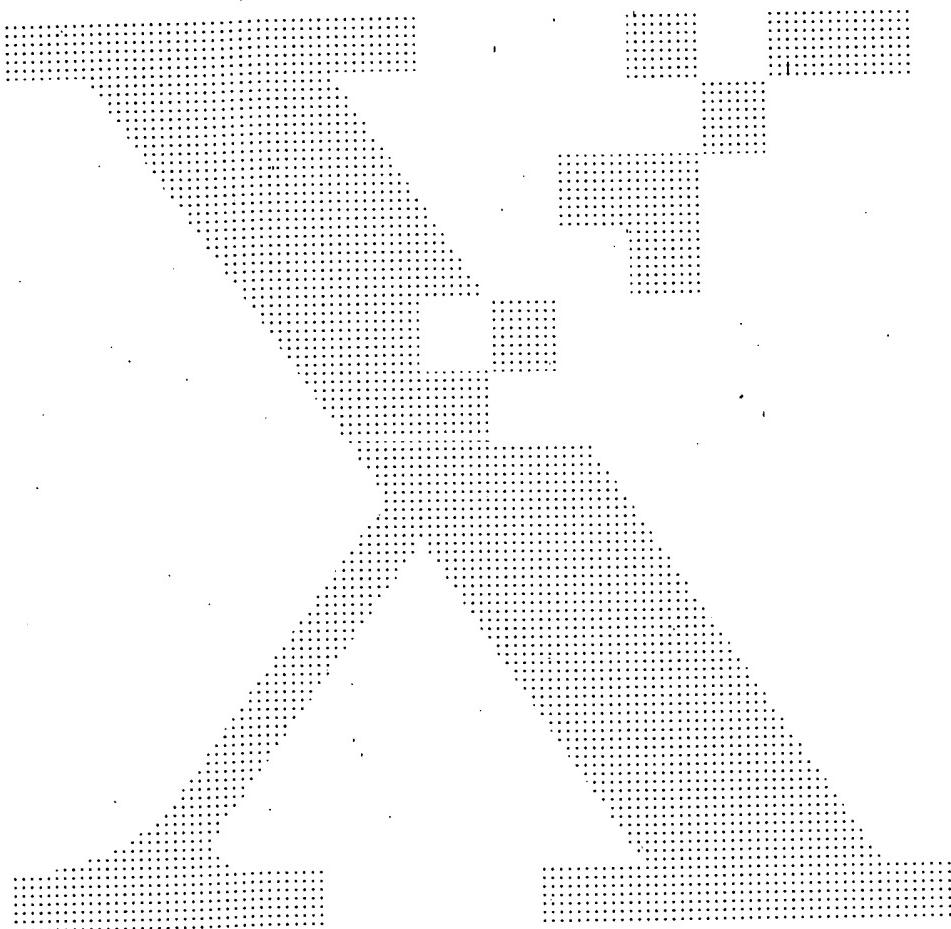
FIG.\_26A

FIG.\_26B

FIG.\_26

# CKochman

<http://www.micropat.com/3536410.PDF>  
08/20/03 10:14 AM



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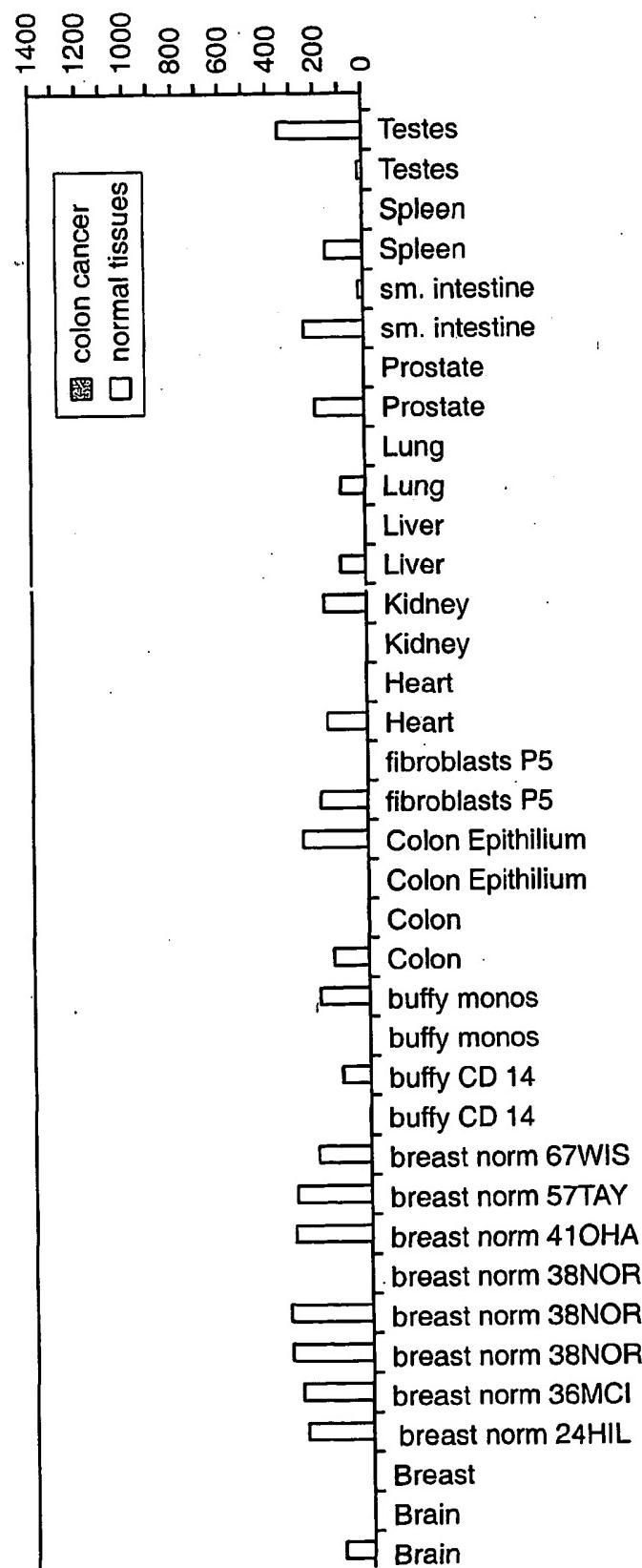


FIG.\_26B

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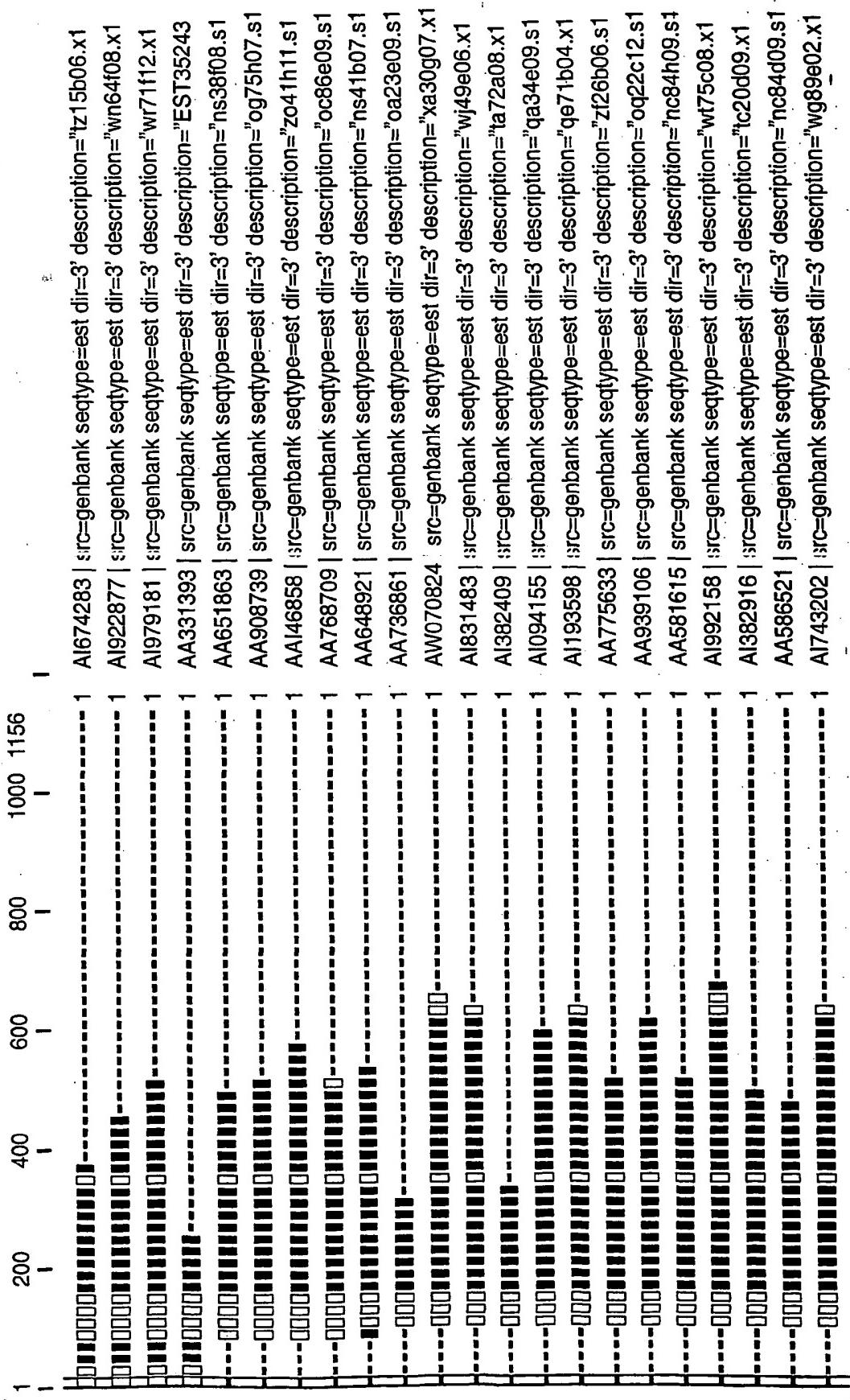
GGCACGAGGAGAACTTAAAGAAATTCAGATATGTGAAGTTGATTCCGAAACCTCGTCA  
 TCCTCTGATGACAGTTGTGACAGCTTGCTTCTGATAATTTCAGAAACACGAGGCTGCAGTC  
 AGTTGGGAAGGCTGTAGGACCCGCAGCCAGTCAGGCACACTGGACCTCTCAGGGTGGCGA  
 TGAAGTTCCAGCGCGAGTACCACTCCGATTCAAAGAGCAACAAAAAGCAGAGTCCCAGGCC  
 TCAGAGAATTCTGTGACTGATTCAAACCTCCGATTCAAAGAGCAACAAAAAGCAGAGTCCCAGGCC  
 GGAGAAAAGGGCTTAAATATAAGCAAAACAAAGCAATGCTTGCAGAAACTCATGTCTGAAT  
 TAGAAAGCTTCCCTGGCTCGTCCGAGACATCCCCCTCCAGGCTCCGACTCACAAATCA  
 AGGAGACCGCGAAGGCGTACATTCCCGGTGTTGCTTCAGGAGAAACCCCTGAACGGAGAGC  
 TCGTCCTTACCGGTCAAGGTCCCGATCTCGGGTCCCTGACGCTCACCCATGGAGG  
 AGGAGGAGGAAGAGGATAAGTACATGTTGGTGGAGAAAGAGGAAGACCGTGGATGGCTACATG  
 AATGAAGATGACTGCCAGAACCCCTCGCTNCAGATCATCCGTGACCCCTCCGATATAAT  
 TCGCCCAGTGGAGAAATACAGAAGGAGAGGAGTTGGAGAACGTCTGCAGCAATTCTCGAAG  
 AGAAGATTATAACCGTTCACTGGGYTCTACTTGTCAATGCCGTCAAAGACTATTGATA  
 CCAAAACAAACTGCAGAACCCAGACTGCTGGGCGTTCAGGGCAGTTCTGTGGCCCTGC  
 CTTCGAAACCGTTATGGTAAGAGGTCAGGGATGCTTGCTGGATCCGAACGGCATTGCC  
 GCCTGTGAGGAATCTGCAACTGCAGTTCTGCCGGCAGCGAGATGGACGGTGTGCGACTG  
 GGGTCCTGTGATT~~T~~CCAAATATCATGGCTTGGGAATGTGCAATGCCACTTGAAGA  
 CTGAAACAGGAATTGAAATGCAAGCATAATATCTGGAAAATTGCTGCCTGCCTTACTT  
 CTCAAATCTTCTTGAAAGTTCCAATT~~T~~~~T~~~~T~~~~T~~ACTGAAACCTGAGT~~A~~AAATCTTGA  
 TGATCAGCCTGTTCATAGAAACTCCAATCAAGTTAMTCTTAGCAGACATGTGTTCTGGA  
 GCATCACAGAAGGTATATTGCTAGTTACACTT~~G~~CCCTCTGCAGTTCTCTGCTCCCA  
CCCCCATCTCATAGCATTCCCCCTATTTCCATTGCTCCCTCCCAACCCGCTTAAGT  
TTTCTGAATT~~T~~TTTAAAWTTACAGTTAAGGAAAAGCCATATT~~T~~TTAC~~T~~GGT  
GTTGGAAATAGCCCTCCATAAAACCTAAGCACTTGGAAACACAATAATAGTATTAACCTA  
ACTAGATCCTATTGAATTTCAGAGAAGAGCCTCTAAC~~T~~TTGTTACACAAAAGAGTATGA  
TTTAGCATTCATACTAGTTGAAATT~~T~~TTAATAGAATCAAGGCACAAAAGTCTAAAACCATG  
TGGAAAATTAGGTAATTATKGCARATTGAKGGTCYCAATCCCAYGWATKGS~~G~~CTTATGK  
TACMARKKGKTGTCMCAGTTRAGACYTAATT~~C~~YCTAATT~~T~~CTCYGSCCGAAGGKWAAGK  
GGKGCGTCCRGTTACMCATCATATT~~C~~MAAGGKTGGKGGS~~A~~TGTAAYMCTTAATTAAA  
ATAATKRWGGAAAGAGCYATCTGGAGATTAWGAGTAAGCTGATTGAATTTCAGTATAAAAC  
TTTAGTATAATTGTAGTTGCAAGKTTATT~~C~~AGTTCACATGTAAGGKATTGCM~~A~~TTAAAT  
TCTTGGACAATTGGKATGGAAACTGATATTAAAAGTAGTC~~T~~GTGGKT~~T~~TTGCAGTT  
TTGTAATTTTAAACCAGGCACAAGGTTCAAGTTAGATT~~T~~AA~~G~~CACTTTATAACAATG  
ATAAGTGCCTTTTGGAGATGTAAC~~T~~TTAGCAGTTGTTAAC~~T~~GCACATCTG~~C~~CCAGTCT  
AGTTCTGGCAGGTTCTGT~~C~~AGTATT~~C~~CCCTCT~~T~~TTGCATTAA~~T~~CAAGGTATT  
GGTAGAGGTGGAATCTAAGTGT~~T~~TATG~~T~~CCAA~~T~~TTACT~~T~~GCATATGTAACCAACATTGCTGT  
GCCATTCAATGTTGATGCCATAATTGGACCTTGAATCGATAAGTGTAAATACAGCTTTGAT  
CTGTAATGCTTTTATACAAAAGTTATT~~T~~AA~~T~~AAAATGTTGTTCTAAAAAA  
AAAAAAATTGCGGCCGCAAGCTTATT~~C~~CCWTAGTGA~~G~~KSWTAATT~~T~~AGCTGGCACTGG  
CCGTCGTTACAACGTCGTACTGGAAAACCC~~T~~GGCGTTACCCAACTTAATGCC~~T~~TGCA  
GCACATCCCCCTT~~C~~GCCAGCTGGCGTAATAGCGAAGAGGCCGCCACCGATGCC~~T~~CCCA  
ACAGTTGCGCAGCCTGATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAAGCGGGCG  
GTGTGGTGGTTACG~~C~~SCAGCGT~~G~~ACCGCTACACT~~T~~GCCAGGCC~~T~~AGCGCCGCT~~T~~TT  
GCTTCTCCTTCGCMCGTTGCCGGTT~~T~~Y~~C~~CC~~K~~CAAGCTNTAAATCGGGC

**FIG.\_27**

One position equals 20 bases.

- if more than 2 bases disagree with consensus sequences.
- if more than 10 positions are unknown.
- if more than 10 positions are gap characters.

FIG.-28A-1



-2 AI378205 | :rc=genbank seqtype=est dir=3' description="tc65a07.X1

FIG.-28A-2

FIG.-28A

FIG.-28A-1

FIG.-28A-2

## FIG.\_28B-1

NCI\_CGAP\_Ut2 Homo sapiens cDNA clone IMAGE:22888627 3', mRNA s" srcf=gbclu7/29773  
 NCI\_CGAP\_Lu19 Homo sapiens cDNA clone IMAGE:2450247 3', mRNA " srcf=gbest16/151593  
 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2493167 3', mRNA s" srcf=gbest37/46306  
 Embryo, 8 week 1 Homo sapiens cDNA 3' end, mRNA sequence." srcf=gbest13/573  
 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1185927 3', mRNA " srcf=gbest17/53268  
 NCI\_CGAP\_Ov8 Homo sapiens cDNA clone IMAGE:1454173 3', mRNA s" srcf=gbest21/613  
 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IM" srcf=gbest10/2075:  
 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1356616 3', mRNA " srcf=gbest19/36742  
 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1186165 3', mRNA " srcf=gbest17/50927  
 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1305832 3', mRNA " srcf=gbest18/70299  
 NCI\_CGAP\_Br18 Homo sapiens cDNA clone IMAGE:2568348 3', mRNA " srcf=gbest18/61005  
 NCI\_CGAP\_Lu19 Homo sapiens cDNA clone IMAGE:2406178 3', mRNA " srcf=gbest35/22416  
 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:20" srcf=gbest26/68899  
 Soares\_NhHMPU\_S1 Homo sapiens cDNA clone IMAGE:1688680 3', mR" srcf=gbest26/68899  
 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:17443" srcf=gbest21/35326  
 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone IMAGE:3780" srcf=gbest13/43614  
 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE:1587094 3', mRNA s" srcf=gbest21/28363  
 NCI\_CGAP\_GC1 Homo sapiens cDNA clone IMAGE:797537 3', mRNA se" srcf=gbest16/43395  
 Soares\_thymus\_NHFT1 Homo sapiens cDNA clone IMAGE:2513294 3", srcf=gbest37/59215  
 Soares\_NhHMPU\_S1 Homo sapiens cDNA clone IMAGE:2064401 3', mR" srcf=gbest26/69406  
 NCI\_CGAP\_GC1 Homo sapiens cDNA clone IMAGE:797489 3', mRNA se" srcf=gbest16/48294  
 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:237" srcf=gb:u8/18434

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Soares\_NhHMPu\_S1\_Homo\_sapiens\_cDNA\_clone IMAGE:2069460\_3', mR" src="gbes126/64695

FIG.-28B-2

FIG.-28B

FIG.-28B-1

FIG.-28B-2

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METSSSSDDS CDSFAISDNFA NTRLQSVREG CTRRSQC'RHS GPLRVAMKFP  
ARSTRGATNK KAERSQPSN SVTDNSNSDSE DESGMNF'LEK RALNIKQNKA  
MLAKLMSELLE SFPGSFRGRH PLPGSDSQSR RPRRRTI'PGV ASRRNPERRA  
RPLITRSRSRI LGSLDAALPME EEEEDKTMV VRKERTYDGY MNEDDLPRTR  
RYFSSVTLPH TIRPVEEIQK ERSWRTSAAI LEEKLTIVEW ALLVINAVER  
LLIPPKQTAET QTAGFAEASS VAPAFETVM KRSGMLWIR TGIAVLVEES  
ATAVSAGSEM DGVRIGSLCI

FIG.-29

MAQQLQTRFYTTDNKKYAVDDVPFSTPAASEIADLSNIINKLLDKKNEFHKKHVEFDF  
LIKQFLRMPILDKHMEMENISSEEVVELEYVEKYTAPOPQOCMFHDWISSIKGA  
EEWLITGSDYDXTSRISLWSLEGKSILWTIVGHTDVVKRDVAWVXKDSLSCLLSSAAMDQ  
TILLMENNVERNKVKALHCCRQHAGSVDSIAVDGSGTKFJSGSWDKMILKTIWSTVP  
TDEEDEMEEESTNRPKKQKTEQLGLTRPIYTLSGHMEA'VSSVLWSDAEICSAAS  
WDHTIRWMDVIESGSLKLSTLTGNKVFNCLISYSPICKRLASGSTDREHIRLWDPTRKD  
GSLVLSLTSHTGWVTSVKWNSPTHEQQLISGSLDNIVRLNDTRSSCRAPLYDLAAK  
EDKVLSYDWTDTGFLLSGGADMKLYSYRYSPTTSKVGA.

FIG. 33

MNP CANTVSPWRESESVGIPF  
GEDEEHCTVKSFPEGPAVRLSKDRSTLQVLDSATGNWF  
GPDQDLDVETIENSQELMRNNSGGPCLSGSLVSLHCLACGKSLKT  
HVGGSSTLDPHWVITAHCFRKHTDVTNMVKRAGSDKLGSFP  
PLTFSGTRPICLPEFFDEELTPATPLWIIGWFTKQNGGKMS  
MWCAGIPEGGYDTCQGDGGGPLMYQSDQWHTVGGIVSWG  
EJCGQPLHF1PERKQLCDGELDCPL  
TEAALAETACRQMGGSSKPTFRAVEI  
PRVYGGEEASVDSWPQVSQIYDQK  
AIIIEFPNPMYPKDNDIAIMKLQF  
DSTRCNADDAYQGEVTEK  
SAYLNWVINWKAEL.

FIG. 36

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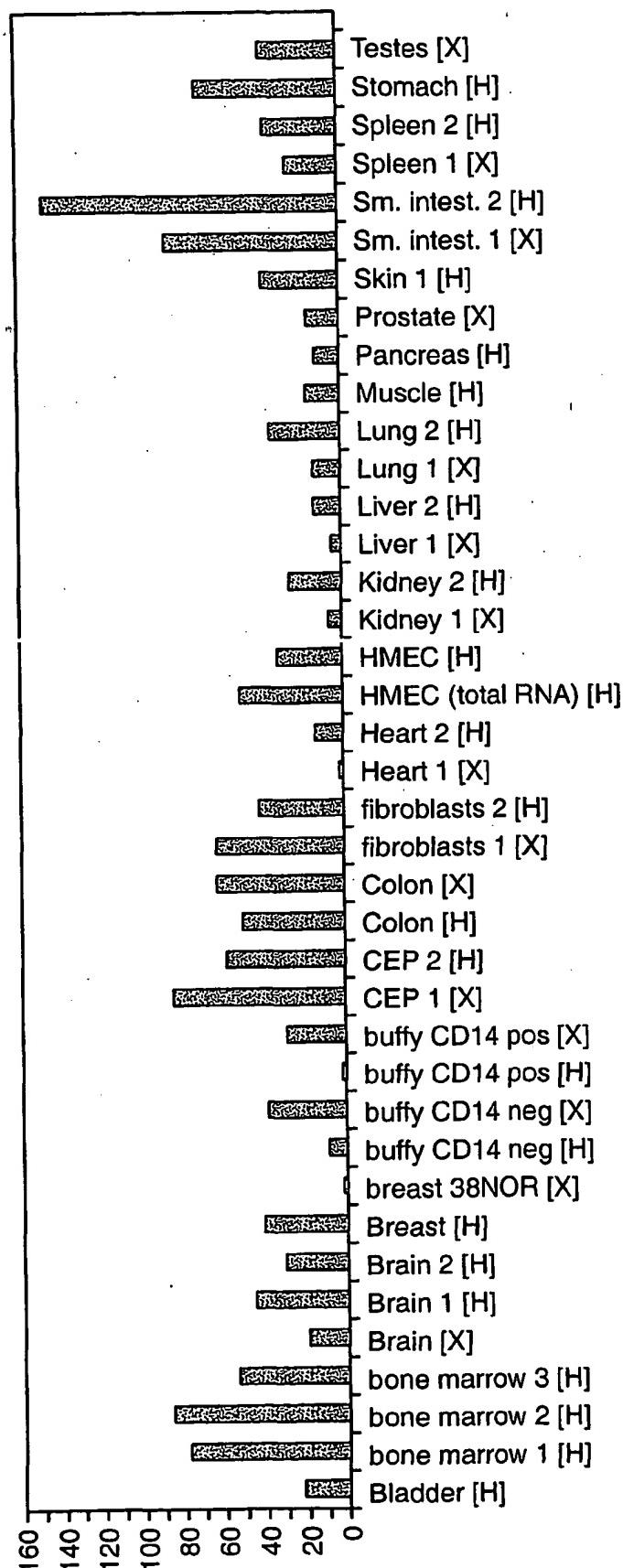


FIG.-30A

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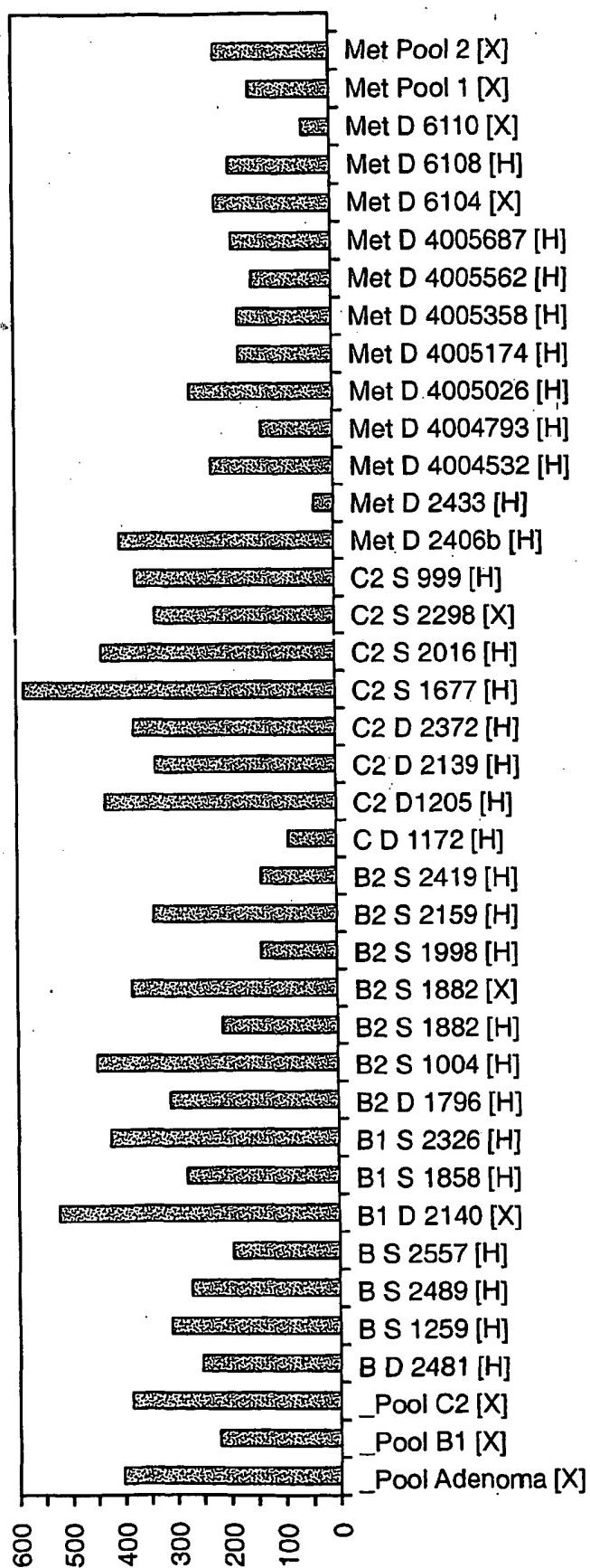


FIG.-30B

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FIG. 31

One position equals 17 bases.

- if more than 1 bases disagree with consensus sequences.
    - if more than 8 positions are unknown.
    - if more than 8 positions are gap characters.

FIG.-32A-1

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1 A1951347(24) | src=genbank seqtype=est dir=3' description="wx67g10.x1  
1 A1952510(24) | src=genbank seqtype=est dir=3' description="wx74g05.x1  
1 A1417099(2+) | src=genbank seqtype=est dir=3' description="lg78g12.x1  
1 AA502337(26) | src=genbank seqtype=est dir=3' description="ne26a03.s1  
1 AA907840(:2) | src=genbank seqtype=est dir=3' description="om16c08.s1  
1 AA528399(102) | src=genbank seqtype=est dir=? description="ne83g12.s1

1 cons for 1

*FIG.-32A-2*

*FIG.-32A*

*FIG.-32A-1*

*FIG.-32A-2*

FIG.-32B-1

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NCL\_CGAP\_Br18 Homo sapiens cDNA clone IMAGE:2548770 3' simila" srcf=gbest37(2)164  
NCL\_CGAP\_Ov38 Homo sapiens cDNA clone IMAGE:2549432 3', mRNA " srcf=gbest37(2)1327  
Soares\_NhHMPU\_S1 Homo sapiens cDNA clone IMAGE:2114950 3' sim" srcf=gbest27(3)3775  
NCL\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:898444 3', mRNA se" srcf=gbest15(4)8530  
SoaresNFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1541198 3" srcf=gbest21(4)257  
NCL\_CGAP\_Ew1 Homo sapiens cDNA clone IMAGE:910918, mRNA sequ" srcf=gbest15(7)499

T T T T T T T T

FIG.-32B-2

FIG.-32B

FIG.-32B-1

FIG.-32B-2

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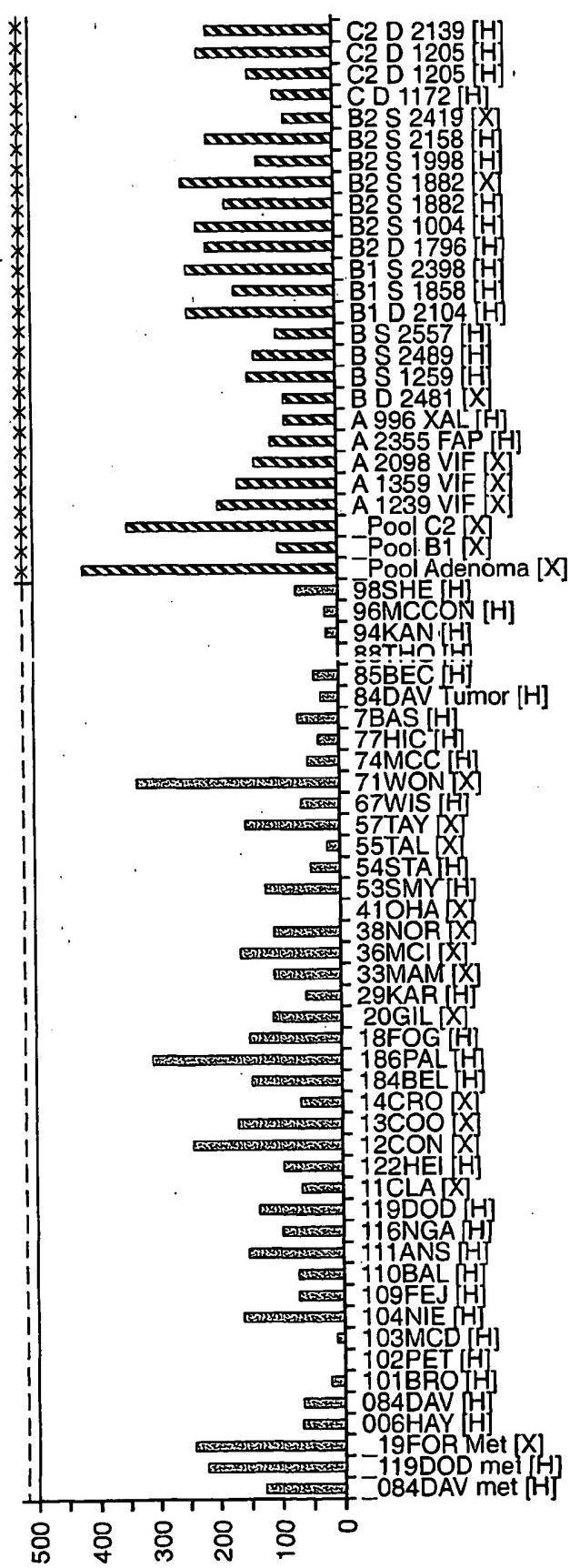


FIG.-34A

FIG.-34

FIG.-34A FIG.-34B

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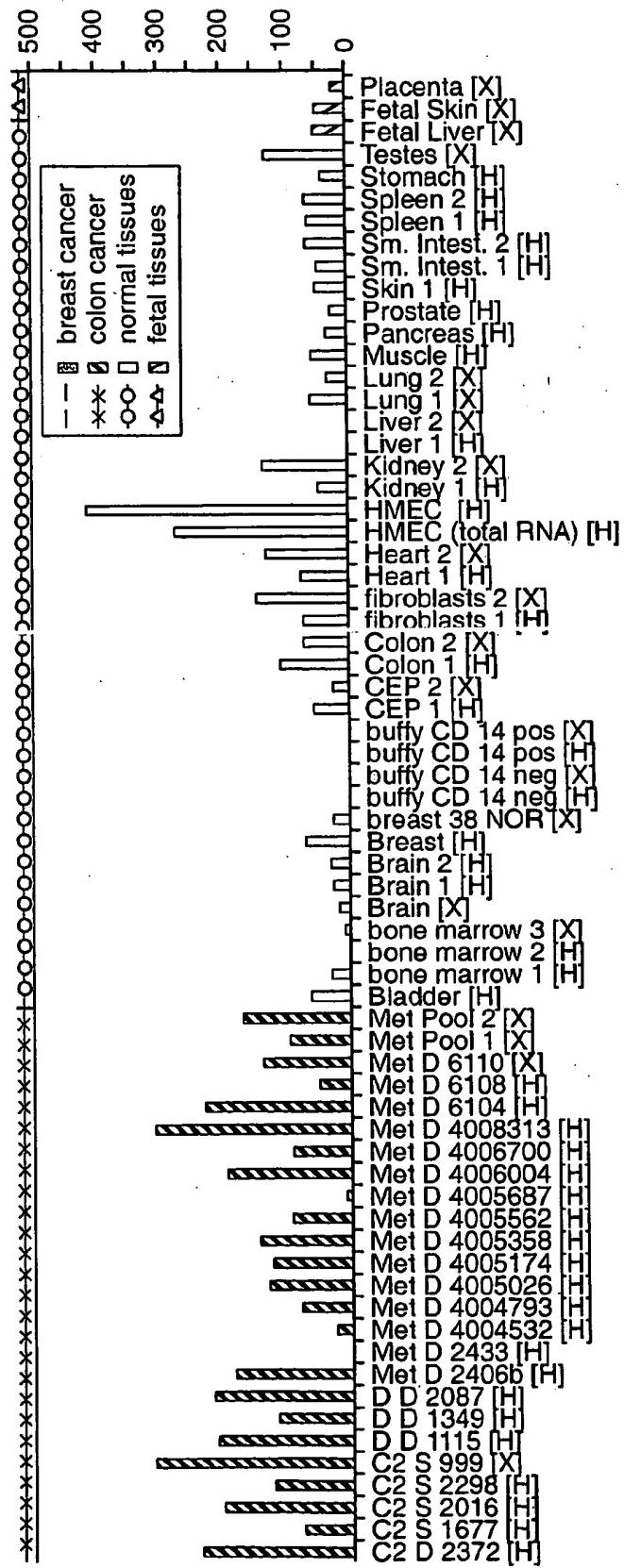


FIG.-34B

GAGGGCAGCAGCTTGTTCAGGGACAAGGATGCTGGCGTGAAGGCCCTGGCACTCGGG  
 CCTCCCTCCAGCCAGTGTGACCAAGGGACTTCTGACCTTGCTCCAGGCTACAGGGAGACCCAGCAG  
 CCTGGCTGCCATTGGGGACAATCTCAGCTCCAGGCTACAGGGAGACCCAGCAG  
 GTACAGGGATCCTGACAGTGATCAACCTCTGAACAGCCTG  
 CCATGGAGACCTTCAGAAAAGTGTGGGGATCCCCCATCATAGCACTACAGCAGCTGGATCATCA  
 TTGTGGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCCTCTGCAGGAGGAGCTGGTCAAG  
 CCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGACTGCTCCAGGGAGGACTGTGTGCAAG  
 AGCTTCCCAGGGCTGCAAGTGGCAGTGGCTCTGGACAAACTTCAGAGCTGGAGATTGGCAAGAAGC  
 CGGCCACAGGGAACTGGTTCTGCTGGCTTCAGAGCTGGTGTGGAGATTGGCAAGAAGC  
 GCAGATGGCTACAGCAGCAAAACCCACTTCAGAGCTGGTGTGGAGATTGGCAAGAAGC  
 GTGAAATCACAGAAAACAGCAGGGAACTGGTCTGGCTTGCTGGAGGCTGAGAACAG  
 TGTCCTCCCTGGCACTGTCTGGCTTGGCAGGTCAAGCATCAGGAAACAG  
 CTCAGGGATTCTGGCTTGGCAGGTCAAGCATCAGGAAACAG  
 CTGGACCCCCCACTGGTCCCTCACGGCAGGCCACTGGTTCAGGAAACATA  
 TGCGGGCAGGCTCAGACAAACTGGCAGCTTCCCATCCCTGGCTGTGGCAAG  
 CAACCCCATGTAACCCCAAAGACAATGACATCGCCCTCATGAAGCTGGCAAG  
 ACAGTCAGGCCATCTGTCTGCCCTCATGAAGCTGGCAACTCCAG  
 GATGGGGCTTTAGGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCT  
 TGACAGGCACACGGTGAATGCAAGACGATGGGTACAGGGAAAGTCAAC  
 ATCCCCGAAAGGGGGTGTGGACACCTGCAAGGGTGAAGCTGGGGCCCT  
 GCCATGTGGCATGGCATCGTTAGCTGGCTATGGCTGGGGCTATGGCT  
 GGTCTCAGGCTATCTCAACTGGATCTACAATGGTCTGGAAGGGCTGAGCT  
 GTGCTGGAGGGCTTCTGCCCTGCCACAGGCTCAGGATCCCCAAAGTCAAG  
 CCCCTGGTACACCCCTCTGCCACAGGCTCAGGAGGAAAGTCAAGGGTAT  
 AGAGACCCCTGGCAGGGCAGAGGGAAAGTCAAGGGTCTCAAGGGTAT  
 AGCATCCAGGGAGACAGGCCACTGAACAAGGTCTCAAGGGTAT  
 CCCACACTGAATGGAAGCAGGCTGCTCTGTAAGGCCAGATCACT  
 AAGGGTCTGGCCAGCCCTGTCGGCTTCAACCCATCCCCAAGGCTACTA  
 ATAAAATGCACTGCCCTACTGGTGTGACTACGTTACCTACTGTG  
 CCACTATTATAAGAGCTGTGTAACATCAAAAAA  
 +-----+-----+

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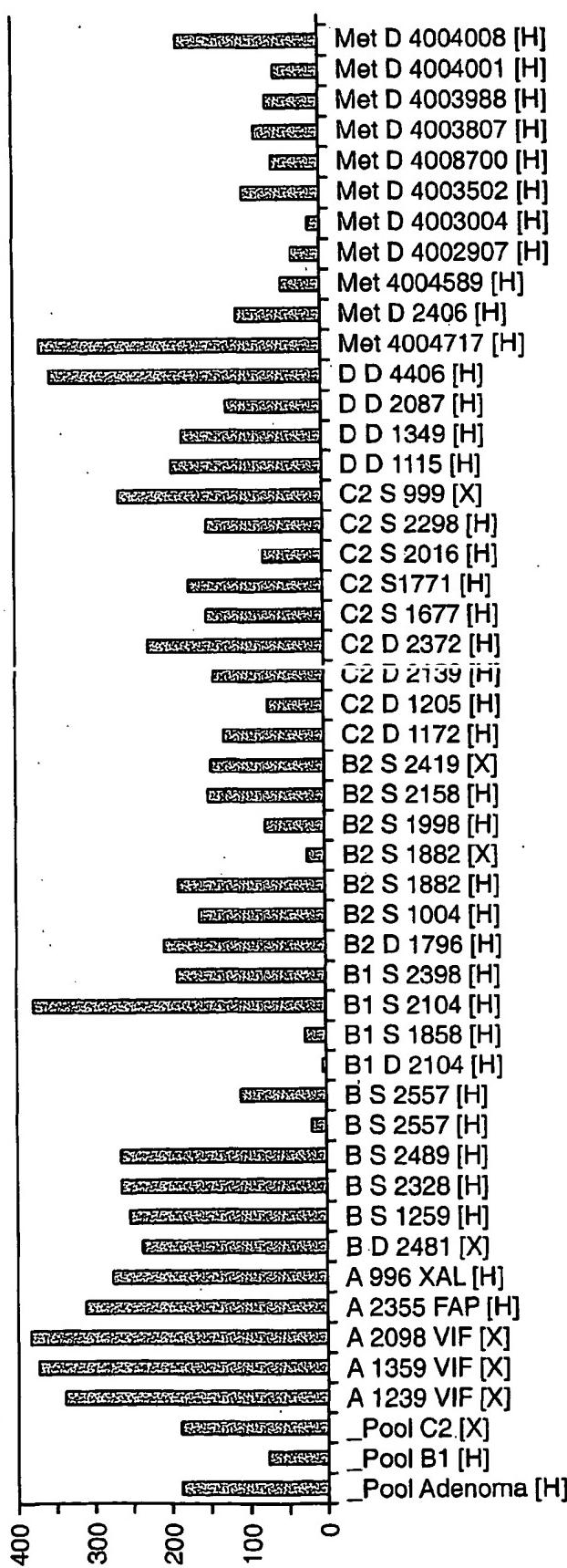


FIG.\_37A

FIG.\_37

FIG.\_37A FIG.\_37B

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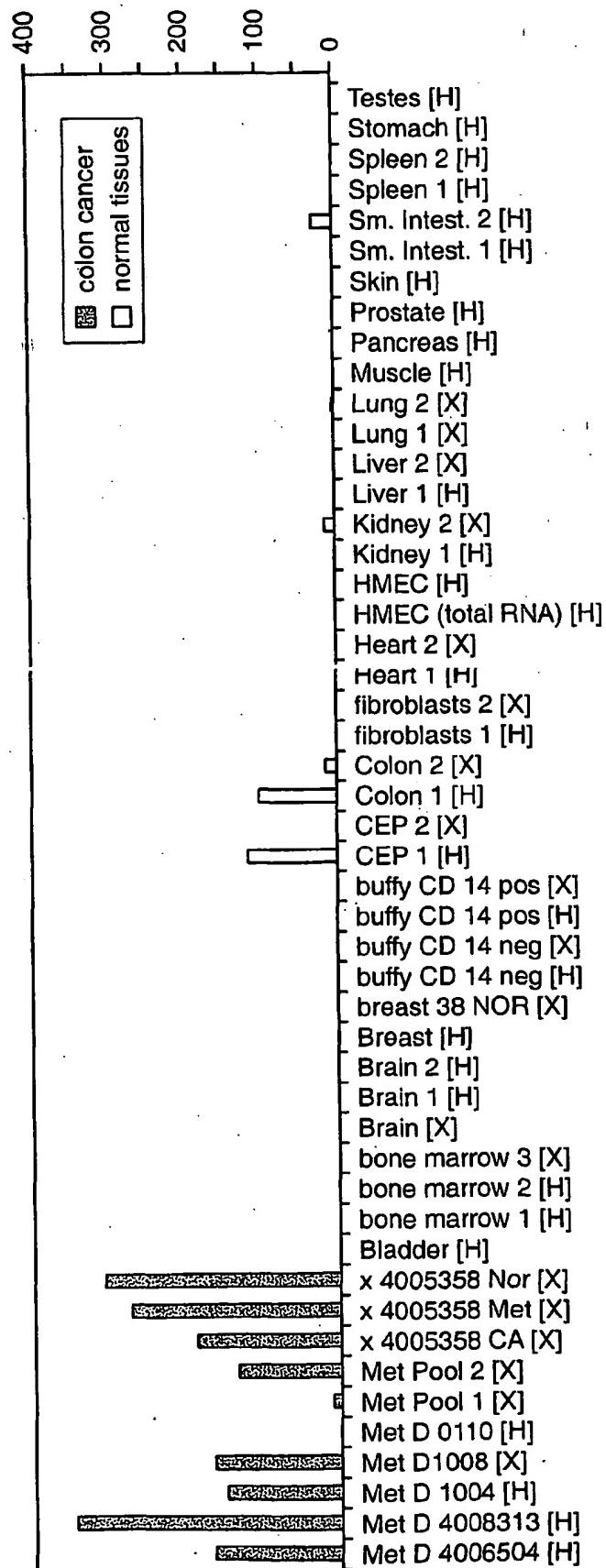


FIG.\_37B

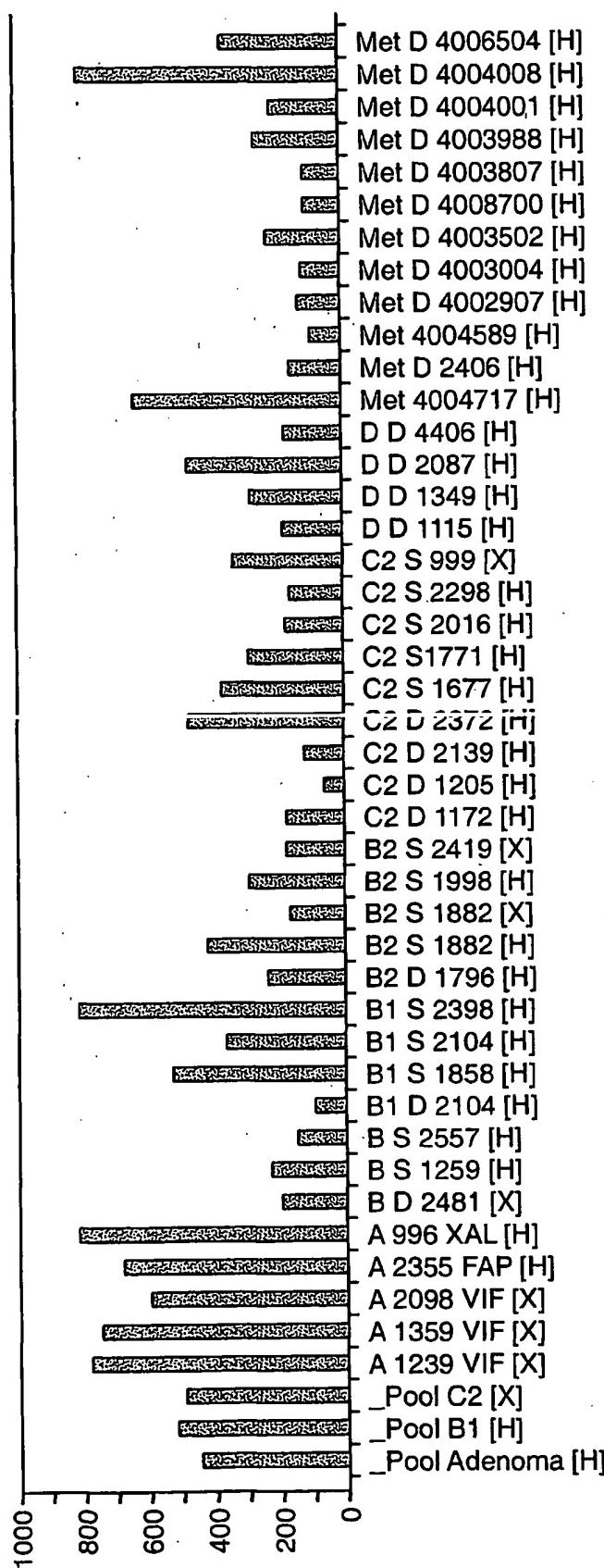


FIG.-38A

FIG.-38

FIG.-38A FIG.-38B

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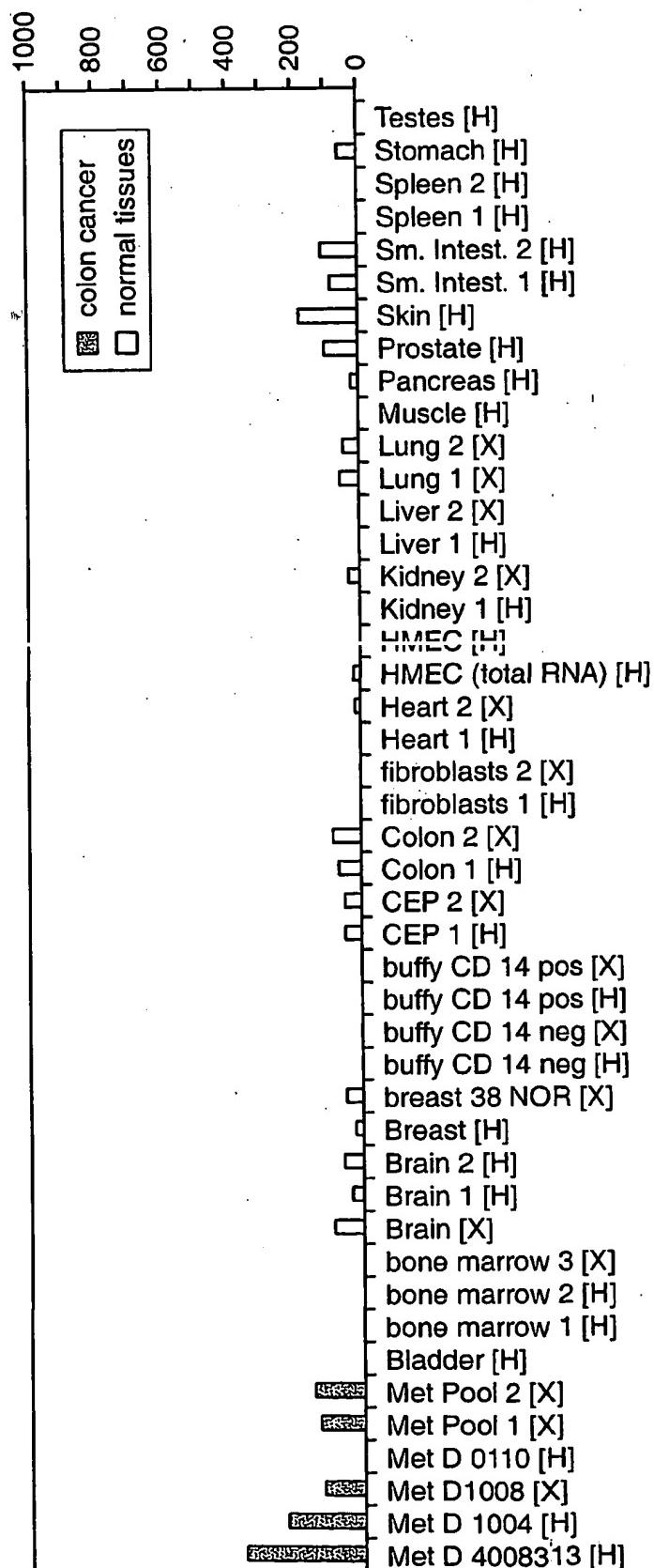


FIG.-3813

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FIG.-39

GGAAATTATAAGATCTTGATAATTGAATCCATCAAGTGGATTCAAGAGATACACCTATTGCCCCTAACAAACCTTA  
AGATGTATTTGGTTATGGAATCATGTGTGGATAGGTCTTAAAGACCTGTTCTCAAAATCTTGACACAGTT  
TCACAGGGTGGCTTATTGACTTGCACGGTTGGCAGATAATCCAGATTACCTAAGATTGGTAAAGGTTAAAAAGT  
CATCTGTGACTTGGCTGGCAGGGCATTTGCTAAGTGGACTCACGGATCTAAAGGGTTCTTAGAAAGGG  
CAAATATTGTCCTAACATGAAGTAAGCAGAAGGACTCTGGGTAAAGCAACAAAACCTGGTGAACCTTA  
CTCTCCACTGCTCTGCAGCTGGATGGCTGATGGCTGATGGCTGATGGCTGATGGCTGATGGCTGATGGCTG  
AGTCCTCCAGGTCACTGTATAATTGCAAAATGCCAGCTCTGGAAAGCAAGTATCATGTACCAAAATGCTTTA  
CTTCTTAACGTTATAATTGCAAAATGCCAGCTCTGGAAAGCAACTTGTGTAATAATGCTCTTAGATGTTGG  
TACACCATTACATTCACTGAAATTAGCTGATGGCATTTAGCATGAAATTTCATTAAGGTTACATTTCAAAATGCTT  
GAGATGTGATTATTTCATATTTCATTAAGGTTACATTTCAAAATGCTTACATTGAGACAAAC  
GAAAAA.....

**FIG.-47**

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**FIG.-40A**

CCAAGTCTACCTCATGTTGGAGGATCTTAGCTATGCCCTCGTAGCTGGCTCCCTGTTGCTGG  
 GGCTGTGGGAACACTCCTTCAGGAGGGCAGCCCTCATCCACAGATGCTCTAACAGGCTGGAAATTATGAA  
 TTGCCCTGCAACAAATTATGAGACCCAAAGACTCCCATAAGCTGGCATTGGCATTCTTGAACTAGT  
 GCATATCTTCTCTATGTGCTACAGCCGGGTGATTTCCAGAAAGATACTTGTGAGAAAATTCTACAGAAGG  
 CATAATGAAATTGATTCTATGCTGTGCTGGTATTCTGATGCCCTCTGGTGGGGTATTCTCT  
 GCAGGGATTATTCTATGCTGTGCTGGTAAACAAATTGTGGAGAAATGACCGAGACAGAACGGAAAATGGCCCTTC  
 TTGTATGTGTCGTTGCTTAAGCAAGCCAGAAACTGTAATCTCCCTGTTGGTATTGTGTTCTATGGTT  
 TGAGGAATGCTTGCATTCTCCCTGTTGGTATTGTGTTAATATAAGCATTGGCATCTCTCTATGGTT  
 GTGGCAAAATCACAGGTAAGAACCCGGATCAAAAGGAGTCGGAACACTGGCAGATAGCAATTCAAGGACT  
 GCGAACTCTCTGTGAATGAAACTCCAGGCAAATCAAAATATAATTGGCCCAAGGCTTACAACACTACCAAGGACA  
 AGGGCTCACAGATCTGAACAGTATCAATTCACTGCTAGGAGGGGAATTCTTGACCGACTGAGACCCAAC  
 ATCATCCCTGTTGATGAGATTAAAGTCCATGGCAACAGGATCAAGGAGACCAAGGGCTTACAGCTGACCCGTGAAA  
 CATGAAACAGCACCTTGAAAGAGCTTGCACCAACAAAGTACACAGCTTACAGCTTACAGCTGACCCGTGAAA  
 CTAGCCCTGGGTCACTCTCAATGACCCCTCTGTGCTGGCATTCAGGTACAGGCTTACAGTGAACACGGCATC  
 AGATTGTCCTAAGCCAGCTGAATAGCAACCCCTGAACCTGGCAGCTCCACCCGGATGCGAGAACTTGA  
 AACGTTAATAACGTTCTTAGGACAGATTGGATGGCCTTCCATTAGGATAATCTCAGGCTTACCTACAGGCT  
 TACCTGACAGAGTACAACGCCAACACAGGACTGTCGTAGCAGGTATCAAGTGAACGGCTTACATCCCTTAATGATA  
 TCAGATATGACAAATGTAACCTAGCGTCTTACCTACATGGAAAGAGTATGATTGATCATTTGTTTATGGTAA  
 TAACACTGAAAGTTACATCCACAGAAATTACAGTACAATGGCAACAGGCTTACAGGCTTACAGGCT  
 GCCTGGTCATCTGCTCTGTGACCCCTCATGGTGTGATTTTACTACCTGGCTTACTCTCAGGCTTACGGT  
 GGCTATGACAGGGCATGCCAACCCGACCCAGGGCTGTGCTCCAACACCCGGAGGGCTCTGGTTG  
 TGGAGTTGGATTAAAGTAAACTGATCTGTGAACCTTACAGGAGCAAGGAATTATCCGGGGTTGGATAACACCCCTAC  
 CAAATGTTGGAAAGACTGGGAATACTATCTCTGGGAAGCTATTAAATAAATCAAAATGAAGCTCACTTT  
 TTACTAAATGAAAGACTGGGAATACTATCTCTGGGAAGCTATTAAATAAATCAAAATGAAGCTCACTTT  
 TGAAACAAAGTTACAGTGAATGGCAAAAGGACTTACGGCACTTACGGCACTTACGGCACT  
 ATATCAGTGAACATCTCAACATAATGAGCATAAGCAGTGAATTGGAAAGTCAGTGAAGGTA  
 AATCTTAATATCTTCTGTGGGTGAGGAGAAAACCTCAGGATTGGCTGCTTGTGGAATAGGA  
 CAGAATGAAATTATGACAGCTACTTGGCTCAGACTGGTAATCCCCGGAGGTGAATCTTTATCATTTG  
 CATATGATCTAGAAGCAAAGCAAACAGTTGCCCTGGGAAGAAATTGGCAACTCCCTGAAAGAGATGCA

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**FIG.- 40B**

CAAACTTAAACAAATTCAACCAGCAACCGAGTCCTCCATATGAAACAATCAGCTACTATACCAAAAG  
 CGTCAGATACTTCACAGCACAGGGAAATGGATTGTGGAGAGAGTAACTAGGATTCTAGCTCTCTGGATT  
 ATAATAGGATATTGAAACATTACAAACAACTTCCCTCTGTATTATTGAGGAACACTAAGAAGTATGGAGAACAA  
 ACCTGTGGCCACCAGCTCTAGATACTGCTGTGATGTGTTCTGTGTAGCTACATTATGCCACCCCTTGAAATT  
 TGTTTGGTTGGCATAGGAAAGCTACTGTATTCTCCGGCTCTAACTTTTGC GGTTAAACTGCGCT  
 AAGTACTATCGTCGAATGGATTGGGGACGTGTAGATGTAACTATACCCATGAAAAAATATGGA  
 AAATGGTAATAATGGTTACATAAAAGATCATGTATATGTTACAAATCCTGTTATGACAAGCCCCATCAC  
 AACAT**GA**TAGCTGATGTTGAAACTGCTTGGACATCAGGATACTCAAAGTGGAAAGGATCAGAGATTGG  
 GTAGTTCTGGGTCTACAGGACTTCCAATCCAGGGCAACGCCAGTGGCAACGTAGTGTGACTCAGGCC  
 GCACCAAGGCAACGGCACCATGGTCTCTGGGTAGTGGTTAAGAATGAAACACAATCACGTTATAGTCCAT  
 GGTCCCATCACTATTCAAGGATGACTCCCTCCCTGCTCTATTGTTTACACTGAGT  
 TTCTATTAGACACTAACACATATGGGTGTTGTCATGGATGCATTCTATCAA  
 TGTGATGGCTAGATTCTACATATTGCCATGTGGAGGTGTGCTGAACACACACCAGTTACAGGAAAGAT  
 GCATTGTTGTAAGTAAACGGGTGTTATACCCATTGACTTCTGGCTGTTGAAATAATCCATT  
 AGGACTTTCTTCTAAATGAGCTAAATAAGTCACCATTGACTTCAAGCAGAGATTTCATCTATTATCAAGAT  
 ACTAAAAGTGTGAAACCTACAGGATATTCTCAAGGTTAACAGAGTTTCACTT  
 TGGCCCATGTTCCACTTGGAAATGGCATGCCAAAGCCATATGAGAAACCTGGCTAACCTGGCTAACATTCTGACAA  
 TTCAAAAGAGAGAGAGATCTGAGAGAGAAATGCTGTTGCTGATTAGGATAAACATTAATTGGAGTGCA  
 CAATTACGGGTACAGTTAACAGAGTTTCAAGGTTAACAGAGTTCTGTTGCA  
 TGAGTATCAGACTAGTATCAAGTGTCTAAATGAAATAATGAGAAAGATCCCTGTCACAATTCTTAGATC  
 TGGTGTCCAGGATGGATGAAACCTTGTAGTTGGATCTGTCATTGAAAGCA  
 TTTGCCTCAGGAGTTCATGTTGGATCTGTCATTCAAAAAGTGTAGCA  
 AATTAAACGGTTGAAATGGAAATTCCAGATGTAGGCAATTCCCCCAGGTCT  
 TTCTGATTCAATTGAAATAAAAGGAACATTGGAGTTTCACTGTCAGGAGTTGG

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GATTTAATCCTATGACAAACTAAGTGGTTCTGCACCTGTTT3GTGAGGTGTTGAAGAGTTGGT  
 GTTGCTCAGGAAGAGATTAAAGCATGCTTGCCTTACCCAGACTCAGA3AAGTCTCCCTGTTGTCCTAG  
 CTATGTTCCCTGTTGCTGCAATTGGCTCAGGAAACCGCC3AGAGTAGAACGTTGATCTGGCTCACCGTCC  
 ACGCTGAGACGATCCTGGGGTGTGAACAAACACTCACCAGGATTTGAAAGATCTGGCTCACCGTCC  
 TCTTCATTTTCCGATTATGATCCTCGTTGCTGCAAAGGGAGTGGCTACGAGTGGAGATGAGCCGGACTT  
 TGCTGCAACACCCCTGGCAGGGCTGCAAGAACGTTGCTAGCTCGGGCTCCTAGTGGCCATGGCACGTT  
 CGGCTATGGCCCTGAGCTGATCTCGTGTCCAGGCCAGGGCTCAGGGAGATAAGAGT3AATTAAAGGACATCGAGGGAGAT  
 GGAGACATGAGAAAGAGAAAGGGATCATCAAGGGGGATAAGAGT3AATTAAAGGACATCGAGGGAGAT  
 CAAAACCCAGAAGGGTCCGATCGAAGGGTCCCCTGGGACCTAACACAAGCAGCATCTTCGGGTC  
 ATCTTCGAAGGCCCTGCGCTTCACTGAGCTCTCTATGTCATGAGCTGCTGACTGTAATGTCAGTAATTGGTTATTGCTA  
 AGTGCACAGCCCTGCGCTTCACTGAGCTCTCTATGTCATGAGCTGCTGACTGTAATGTCAGTAATTGGTTATTGCTA  
 CACAGTGTTCATGATTGGCAGTGTCTGGAAATTGGCATCTGGTAATGGTCACTGAATTGGTTATTGCTA  
 ATTAGATATTGTTCTGGGAAGTCAAAAAGCCAGT~~TAA~~  
 ACAGCATGAGAGGGATGAGGCAACCGGTGCTAGCTGTCAGGCTTAATTCCTGTAAGGCTCAGGTAAACTCCAGATGCCAACATAG  
 AGATTCTGACCTTAATGCAACCATTGCAACCTTAAGCTCAAAAGGCCTAATTCCTGTAAGGCTTAATTTCCTTAATTGCTTCACTTAAG  
 AGCTCTGCTCCCTAAAGCCTCAAAACAAAGGCCTAATTCCTGTAAGGCTTAATTGCTTCACTTAATTGCTTCACTTAAG  
 TTAGTTCCACTGAGACCCAGGCTGTTAGGGGTTATTGTTGTAAGGTACTTTCAATTGTTAAACAGAGGA  
 TATCGGCATTGTTCTCTGAGGACAAGAGAAAAAGCCAGGTCCACAGGACACAGAGAAAGGT  
 TTGGGTGTCCTCTGGGGTTAACCTCTAACAGTGGTATGTTGTAATGGTATGTCATTGCTACTATGATTAAATTGCAATT  
 GCTTGGGAAGTTAACCTCTAACAGTGGTATGTTGTAAGGAAATTAGGTTAACAGTGGCTAACCTTAAGCTTGGTACACTTTGGGA  
 AGTGA AAAACTTGTAGTTGATGTTAACAGTGGTATGTTGTAAGGAAATTAGGTTAACAGTGGCTAACCTTAAGCTTGGTACACTTTGGGA  
 TTGTTCAAGGGCTCAGATTGTAATATGTAATTAGTGAATTGTAATTTGTTGTAAGGAAATTAGGTTAACAGTGGCTAACCTTAAGCTTGGTAC  
 GCCTCATGTCAAAATTAGTGAATTGTAATTGTAATTTGTTGTAAGGAAATTAGTGAATTGTTGTAAGGAAATTAGTGAATT  
 TGTAATGACAGGCTGTCACAGCTGAGAGGGCTGTCAGGAGACTAGAACGACTAACCTTGGTACACTGGCTAACCTTAAGCTTGGTAC  
 ATTTAAAGAGGTGAGCTGGAAATTGACACAGTACCAATTAAAGCAGGTTGGAAAGACTGGACTCTAACCTGTTGATTAAAG  
 ATGAGGCTTGGCTACCTTCAAGGGAGTTCTGCTGTTAACAGGAGTTGGAAAGCTAACCTTAAGCTTGGTACACTGGCTAACCTTAAGCTTGGTAC  
 ATAACATAAAACATGTAAGGAAATTGAGGAAAGCTAACATTGTTGTAAGGTTAGATAAATTGAGGAGCTAACATTGTTGATTAAAG  
 TGAACCTGAAATAAGCTGCTTCAAGGAAATTGCTGACATGGTTCCAAAATGGTACTCCACATACTTCAGTGAGGG  
 TAAGTATTTCCTGTTGTAAGGAAATTGCTAACATTGTTGTAATAAAAGGATTTGTAATGTTGAAATAGCTTAAATGA  
 TATGCTGTAACCTAAATAATTGTAATGTTGTAATGTTGAAATGTTGTAATGTTGAAATGCTTAAATGA

FIG. - 42

T

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CGGCCAGGCACACCCCCGGCACTCCTCGGGCAAGCTGCGCCCTCGGCCAAGGGCAAGTGGCCAGTGGCCAGGGCTGGGGCTGGGCCCCGGCT  
 GAGTGGGTGTAGCTGGCCTCGGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCT  
 GCTGGCCAGCTCTGCACGGCTGGGGCTCTGCACGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCT  
 GGATAAGGGCCGCG  
 CTGGGCGGTGCCCGCTGCCTGCTGCCTGCTGCCTGCTGCCTGCTGCCTGCTGCCTGCTGCCTGCTGCCTGCTGCCTGCTGCCTGCTGCCT  
 GGAAGTCTTCAGGCCAAGTTTCACACTTACAAGGGACTGCGTATCTTACACGGTTTACACGGTTTACACGGTTTACACGGTTTACACGGTTTAC  
 TGGAAAGTCCAGAGATACTGGTGTGCTTTACACGGTTTACACGGTTTACACGGTTTACACGGTTTACACGGTTTACACGGTTTACACGGTTTAC  
 AAGGGTGTGACCTTGAGGTTCATCGGGTGTGATTGCCCCTGATTGCCCCTGATTGCCCCTGATTGCCCCTGATTGCCCCTGATTGCCCCTGATT  
 CGAGACACATCACTATTCACTATTCACTATTCACTATTCACTATTCACTATTCACTATTCACTATTCACTATTCACTATTCACTATTCACTATT  
 CCAGAACCGCGAGAACATCAACTTCTCATGACTATTGAGGATAATGAGGATAATGAGGATAATGAGGATAATGAGGATAATGAGGATAATGAG  
 TACAAGCGAGAACATCGATCTGTTGCTGGCAATACCGTCAACCTAAAGAGTGGAGGTCACTCCCACTCCTCAGCTGTTGCTGGCAATACCGTCA  
 AGACTCACCGTCCACTCCCTCTCCAAAGCTTAAGCTCACTCCCACTCCTCAGCTGTTGCTGGCAATACCGTCAACCTAAAGAGTGGAGGTCA  
 ACTGATGAACACTCTTTGTATTCTCTCGAGGTCTCTCGAGGTCTCTCGAGGTCTCTCGAGGTCTCTCGAGGTCTCTCGAGGTCTCTCGAG  
 AGTGGAGCTGTGGGACATGTGGGAGGATCCGGCAACAACTGAGGGAGGATCCGGCAACAACTGAGGGAGGATCCGGCAACAACTGAGGGAG  
 AGTACATCAATCAGAGGAAGAGTCAAGGGAG  
 TCATTTTATCTATGGCCCATTTGGATCTGTAAATCCCTATCCAGGTCTCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGG  
 CTGCCGGGGTCCACAGTGTGGATTCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGG  
 GCTTCTGAATGCAATATGGCTTCATCAACT  
 TCCCCTACTCCCTTAGGAGAAATGCCCAGGGTCTGGCCATCAAAGGGTCTGGCCATCAAAGGGTCTGGCCATCAAAGGGTCTGGCCATCAA  
 CATAATCTCTCACAAAGTCCACTTACTCAAAATTGGTGAACAGCTGATAGCAATGTGTTATAGCTGATCAATGTGTTATAGACTGGCTT  
 CTGACTAAGGTGACATAATAGTCCACCTACTTGTGAAATTAGTCAACTTACTTGTGAGGCAATTACTTGTGAGGCAAGGGGGCTCTCCCTCGA  
 TGGATTCTTAAGGTCTCTTAAGCAACACAGCTGAGGCAAGGGAGAAGGGGGCTCTCCCTCGAATGACGTTATGGCAATGACGTTATGGATT  
 AACAGGAATTCTATAGTAAAGGGAGGCTAAATTAACACTTTGACTTACCTTACATTACATTATATATTAGTAAAGTGAACCTAAATCCAACAT  
 CATGCCCTTTAAAGTCTCTTAAGCAACAGGACATTAAAGGACCAATAGGCAAGGGGGCTCTCCCTCGAATGACGTTATGGATTAGTCTGGGA  
 TCATCAGCTGTGTTTAGTTAAACATTGGTTAAATAGATATTGGTTAAATAGTAAATTTATAAGATACTAAACCAGCATACCTT  
 TATGATTAAAGACTATGATTACCTTACATTACATTATATATTAGTAAAGTGAACCTAAATCCAACAT  
 ACTCTGCCAGAGTGTGAAAGCTTAACAGCTGAGACTCCTCATACCTCAGTGGCTGGCCAGAGATGACTGTATTAGCTGGGAAG  
 TTCCCTAAATCACAGGACATTAAAGGACCAATAGGCAAGGGGGCTCTCCCTCGAATGACGTTATGGATTAGTCTGGGAAG  
 ACCAATCTAACAGCAAAATAACAGCTGAGACTCCTCATACCTCAGTGGCTGGCCAGAGATGACTGTATTAGCTGGGAAG  
 GCTACAGTGTAGGGGGAAAGGGGATTGTGTAGTCAGTCAAGTCACTGAGACTCCTCATACCTCAGTGGCTGGCCAGAGATGACTGTATTAG  
 ATGACTGGCTTAACCTCCCACTGCCCTGTCATGTGCTTAAGCCACATTAAAGGAGGATTATTAAAGTGAATTTAAATTTCCTGTACTT  
 TACAGACAGGAAGTTCAGGAAACTTTAAGGAACCTTAAGCAAAACTCTGAAAGGAGGATTATTAAAGTGAATTTAAATTTCCTGTACTT  
 CTTTTTTAAATTAGCAACTTCAAGTATAACAAACTTTGAAACTGGGATAAAGTGGATAAAGTGGATAAAGTGGATAAAGTGGATAAAGTGG  
 AATGAATTTGGTGAACAAAAAAACCG

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CTCTGAGTGTCCAGTGGTCAGTTGGCCTTGCTGGCTCTGGCTGGGGAGGGCTTCACGGGCTACAGGACAGGGCAGCTGAGGCAGAGC  
TGGGACACCAGCCAAAGCCCA3AGGAGCCACAGCCCA3AGGAGCCAAAGCCCA3AGGAGCCACAGCCCA3AGGAGCCAAAGCCCA3AGGAGCCACAG  
ACTTTCAGAAGTTGGCTACGGCAGCTCCCCCTCCCCAACCCCTATCCCGAAGGCCCTCCCTCATGGATCACCC  
TGACTCTCTCAGCATGGCCCTCCCTGGGGACAGAGTCAAGTGCAGGCCCTCCCTGGCTGAAGGAAGTGGTCCAGGAGCCAACTCCCTGTCC  
ACCCCTCTCCAACAGAAAAGCTGTACCTGCCAACAGGCTGCCCTCTCCAGCACCCCATGAAACAGAAAGGAAC  
CTCAGGAAGCTGTCCCCCTCCAAAAGAGCTGCCCTTAACCGTCAAGCATGGTGTATATGGTCCCCTGGAACCTACAGTCAGCTA  
GCCAGGCTCCATTGGGGACAGGCCATCCAGAACCTGAGTCCTTGGGAATGCCAGGCCAGCAGCTGCCAACAG  
GACCGGGTCCCCAAGGGGGTGGGGGCAACCGGGTGGATGGCTTCCCCCTGGGGGGCCTTCTCCAGACAATC  
TGAACCAAATCTGCCTTCCTAACCGTCAAGCATGGTGTATGGTGGAGATTTCTGGAGATTTCTGGAGATTTCTGGAGATTTCTGGAGATTTCTGGAG  
CTCCCCACCTCACTCGGCCAGGGTAGAGACCCCTAACCTGGCCAAACTTGTGTGGAGGAGCAATGAGCCGATTCTGTGAG  
CGCAGCCACACAAACCGCTTAGAGTGTGGCCAAACTGGCCAGGGCAG3GGGAGGCTCGGTCTCTGCT  
CCGAGTCTGGTCAAGACCCGACCCCACTGGTGTGCCACGGGGCAGCTGGCTGGGACTGATGGTGTGGACTGATCCA  
CCAGGAGAAGCTCCCCAGCCACACTACAGCTGGGGCTGCCAACATGCCCTGATAATTCTCTGG  
GGTCTTGGAGCTGGCTTCCCTCCTGGGGTAGTGTGAAGACCCACACTGGACAATATCAAGAACATCTGGCACC  
GCTTCCGGCTCTGTGCCACGCCAACCTGGCAGCTACTGACCCCTTACAAAGGGAGCTGTGGACTGATCCA  
GCTGGGAGGGAGTTCCAGGCGCTGTGCCAGGGGACAATCACACCTGTACATGGAAAGGGCTGGGAG  
GATAACCTGTGACAATAACTGTGACCGGGAGTAGTGTGAAGACCCACACTGGCTCCCTAACCTAACATGACCCGGACATCT  
CTCCCAAGCCCTACTCGGGATGAGTGTGGCTTGTGGGGTAGTGTGAAGACCCACACTGGCTCCCTAACCTAACATGACCCGGACATCT  
GACCATGACATCAGTCAGTCAACCTCATGGGCCACCTCATGGGGATGAACAGGTCAACTGTCTAACATCAATT  
AAGCATAAACATATTCTGGCTGTGACTGACTGACCCAAACTTACATGAAACATGACCCGGACACTGAGAAGGGACTGAG  
AGGCCTGTGTGCCAGAGGGAGAAATTAAACCTTCATCAATGATGTCAGTCAACATCAATT  
GGGAGAACCTGGCTCTGGCTGTGAGTGTGGGGTAGAAGGGCAAGGGCAAGGGGAGCTGAGAAGGGCTCAACTG  
CTGAGGAACGTGGCTCTAGTGTGTGGAGACACTGAGAAGGGCAAGGGCAAGGGGAGCTGAGAAGGGCTCAACTG  
GAGGAACAAATATCAGCTCCACCTCTGAGGCCAAAGGAAGAAATGTCACCCAGGCCCCCTAGAGGGTCAAGGGTCAAGGGTCAACTG

FIG. - 44

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ACTCACTATAGGGCTCGAGGGGCCCCGGGAGGTGGCCACCCACCATCATCTAAAGAAGATAACTTGG  
 CAAATGACATGCCAGTTCTCAAGGAGAATATTGAGAACTTCAACCAGGATACTTCAAGGAAATCAGGA  
 GACGGAGACATTGTCACTTTCGCAACATTCGACCAATTACAGGAACTTCAAGGAAACTCCAGAAATCAGGA  
 TGGCTGCTCTGGCACAGAATTGCTGGGAAGCCCTCTGTTCGACTGTCAGATCCCCGAGGTTCAAGGGACGG  
 ATACAGCAGAACGAAAACATCCGACCCACATTATTCAGGATGATCAAGATGGAGGCT  
 GGGTCCTGCAAGTCATGAACAAACGAGAAAGATTGGAACATGGAACTTGTGCTTACGGGACCTTCATCAATGCCT  
 TTGTAACCTACCCATGTGCTGCCGTCAACGGTCCCTCCATGCTCACCCGGAACTATGTCACAATCACAAAT  
 GTCTACACCAAAACGAGAAACTGCTCTCCCCCTCGCAGGGCATGCAATGAGCCTGGGACTTTGCTGT  
 ATATCTAACAAACACTGGCTACAGAACAGCCTTTTTGAAATAACCTCAATGAATAATGGAGGCTACA  
 TCCCCCTGGGGAGAATGGCTTGGGATTAATCAAGAATTCTCGCTTCATAATTACACTGTTGTCGC  
 AATGGCATCAAGGAAAGGATGGATTGGATTATGCAAAGGAACTACTTCACAGACTTAATCAGGAACT  
 CATTAAATTACTTCAAGGAAATGTATCCCATAAGGCCGTTATGATGGTGTACGGCAGCAGCTG  
 CGCCCCACGGCCCCGGAGGACTCAAGCCCACAGTTCTAAACTGTACCCCCAATGCTTCCAAACACATAACT  
 CCTAGTTATAACTATGCCACAAATATGGATAAACACTGGATTATGCCATATGACTTGAATTGCTGTGCC  
 CCACATGGAAATTACAAACATTCTACAGGGCAAAAGGGTCCAGACTTACATCTACACGGACCAATGCTGCC  
 AGAGGGCTGATAACATGCTGGGAGACGGGGAGCTGGAGAAATCCATGCCATATGACTTGAATTGCTGTGCC  
 GGTACCATATGGGAGTTGGCAGTTGGACTGGCTCAAGGGCAACAGGTTTCCAGGATCAAACTGGCTG  
 TTTTTTATTCTGGTCCAAGTGGATATTGCTGGCTCGACACCCCTGTATGGACGCCAAGTCTCAACATTG  
 CCCACAGATCCCTGGGATACATCTGGCAAGGCTTCAACAGGTTTCCAGGCAAAAGGGCCAAATTTGGGT  
 CTGGACCCAGAAAAGCCAGGTAAACAGGTTTCCAGGCAAAAGGGCAAAAGGGCCAAATTTGGGT  
 AGTGGAAAGGGCAAAATTCTACGTAAAGGAAACTATGCCAGCAGGCCAGGTACCAAGTCCAGGCAAAAGGG  
 CCAAATATGAAAGGGTCAAGGAACATCTGGGATACATCTGGCAAGGCTTCAAGGTTCAACAGGCTG  
 AACTGGCAATGCCATTGGGATACATCTGGCAAGGAAAGAATGCAAGGCTTCAAGGTTCAACAGGCTG  
 CACAGTCCGGCAGGACGGGGAAACCTCTACGGCTCGGGCTCCATGACAAGGAGTGAAGTGG  
 GGGAGTCTGGTACCGTGGCCACCTTGTCCATACTCGGCAGACAGGTTCTGTGAAATTGAGGTGA  
 CCAAGGTAAGGCCAGATTGTGAGAGAGAACTGTACAATCGCCAGAGCGTGGAGGACCATAG  
 ATATGACATAATTCTGGAAAGAAGAATTAAGAATTAGAATTAGAATTAGAAGTGAAGGAG  
 ATGAAGGCCACAAGGGCCAAGAGATCTCCAGGCTTCCAGGTTCCAGGCTTCAAGG  
 AGCAGCAACGCCAGGGCCACCTTACCTGTCCGAGTGCACACAACTGTGTTTCTCAAGGAGAAC  
 TATCCATTGTGAGAGAGAACTGTACAATCGCCAGAGCGTGGAGGACCATAG  
 AGATGGAAAGCTCTGGCAAGATAAAATTAAGAATTAGAATTAGAAGTGAAGG  
 GAGGAATGTAGTGGCAGTAACAAAGCTTACATAAGAGAAAGGTGAAAAAG  
 AGCAGCAACGCCAGGGAGGAAAGGAGAGAGAGAGAGAGAGAGAGAGAG  
 TATCCATTGTGAGAGAGAACTGTACAATCGCCAGAGCGTGGAGGACCATAG  
 AGATGGAAAGCTCTGGCAAGATAAAATTAAGAATTAGAATTAGAAGTGAAGG  
 GAGGAATGTAGTGGCAGTAACAAAGCTTACATAAGAGAAAGGTGAAAAAG  
 GAGCCATCTTCAACCCATTCAAGGAGGCTGCTCAGGAAGTGAACACTTCAAGGAGAAC  
 ACCGTTAGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 CTCACCTGCTTCAACGGCATGACAACACCAGCCAGACAGGGCTGGGATCTTCTG  
 TTGAGTTGCTACTGGCTTTGGAGTATTGATGAAATAACACCTACTGGT  
 GTGAGTTGCTACTGGCTTTGGAGTATTGATGAAATAACAGATCCTTATCAG  
 GCTACAAACGATTAACAGGAAACTTCAAGGAGGAGAGAGAGAGAGAGAGAG  
 F/G. - 45A

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CACACGGTAGAACCGAGGCATTGAAATCAGCTACACGTACAACACTAATGGAGCTCAGAAGCTGTCAAGGATA  
 TAAGCGCAACCCAAGACCTAAAGAATCTTGATGTTGAAATAAGATGGAGGAAGCTATGACTACACA  
 GAGGACAGTTATGGATGGATGGGAAGGTTTCAGCTTCAGCCGGTCTCACTTGAGACATCAACTGGCAAGGCC  
 AGAGGGCTACACAGTGTGAATGAAAACATCTATGAGTACAGACAAAACACTACAGACTTAGCTGTGGACT  
 GGACTAATTACTGAAAGGATTAGATAGAGTATTGGACTCTGCTGAAGAGTCACATAGAGCAAAATAAAACA  
 AATAAGACTCAAACGTCAAAGTGACGGGTCTGGTCTGCTTGAGTAAACTAGACTGAGCTGTCAATGGAGAT  
 GGCCTCTGCTGACTCGAGATGAAAGACCCAAGGGATAAGGTGGGAAAACACCTCATTTGACGCCAGCTGCCAGCTG  
 ACCTTCACAAACCTGCATTGAAACCTTAAGTCCAGAGAGTAAACTTGAATGGAATAACGACAT  
 CCAGAAGTTAACATCATTGAAATTCTGAAACACTGGAGAAAACCGAAAATGGACGGGGATGAAGAGACTAA  
 TCAATCTGGAAACCGATTTCACTGTCGATGGCATGGAAAGAAACTTCCCAGTATGGTGGTCTGGAAAGCTAGAGC  
 CCATTCCGAGGCCACCCGAAAGAAACTTCCCAGTTCAGTTCACTCAGATGTTCAACATGGCCACGGCCAGAAACCC  
 TACCTTCCCTGTCGATTCGGATGGAAAGGTTGACCAAGGTGGGATATTGGGGATTTGGGGTTGGCTTGGTGTGTT  
 TAATTCCAGCATAGCGGGGAAGGAAAGGCTGGGATTTGGGGATTTGGGGATTTGGGGTTGGCTTGGTGTGTT  
 TAGAAGGCAGCGCCCTCTTCACCTCCTCTGATTAGATGAAACCTTCACTTGAGTAAAGTAAAGTAAACAGCTTACCC  
 TCTGTTTAACCTTTTATTGTAACATAAAAGGTAAATCAACGCCACAAACATCCAAAGCTAACCTGGGT  
 ACCTTTGTCAGTAGAAGCTAGTGAGGCATGTGAGCAAGGGGTGGTGCACAGGGAGACTCATCGTTATAATT  
 ACTATCTGCCAAGAGTAGAAAGAAAGGCTGGGATTTGGGGATTTGGGGTTGGCTTGGTGTGTT  
 GTTGTGTTTGTAACCTAAACAGTATTATCTTGAGTAAAGTAAATCTGTTGAGGACATAAGTATAACATGTTATCCAT  
 CAAGATGGCTAGAAATGGTCGCTTTCTGAGTGTCTAAACACTTGACACCCTCTGGTAATCTTCAACACACT  
 CCAC TGCCCTGCGTAATGAAAGTTTGATTCAATTGAAAGCTAGTTGAGTAAATGTTCAATGCGTCAATTTCAGT  
 AGATGATTGGCACTTGGAGATTAAATGCCATGTCTTATTGATTAAGATTGCTATTTGGGT  
 TTATCAGCTCAGCTGTTGACATTAAAGCTTGGCTGTCATTGTGACAAAGTCAAATAACCCCCAGGACACAGCTATGGA  
 TCACATATTGTTGACATTAAAGCTTGGCTGTCATTGTGACAAAGAAATGGTGCATGCTTTACCTCGACTTGCTAAATCG  
 ATTAGCAGAAAGCATGGCTAAATGTTGGTGTGAAATAATAAGTAAATGTTCAATGTTCAAAAWRAARAWNGC  
 CTGCTCTCTGTGCTCTAGCCTCAAGCGTTCATCACATCACCTTAAAGACATAGTCAAAATTGCTTGGGT  
 ATTTCCTGACAGGGAGAAAAGATCTAAAGATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCT  
 AGAAGCTTAATGTTGATAAAAATGACTAGTTTGAAATTACCCPAGACTCTCTCAATAAAAGAAATTC  
 ATGAATGCTCCACAAATTCAACATACCAAGAGTAATTCTTAACATTGTTCTATGTTATTG  
 TAAGACCTTCACCAAGTTCTGATATCTTTAAAGACATAGTCAAAATTGCTTGGGT  
 GAAATATCCTTGTGTTGATTTAGGTTTAAATAACCGCTAAAGGATTACCTCACTGAGTCATCAGTAC  
 CTCCTATTCAAGTCCCCAAGATGATGTTGTTGCTTCAAGACAGGTTCTCTTATTGATA  
 ATTCAAGTGTGTTGATAAAATTATGTTCTTAAACTTTAATGTTTAAAGAAATTTAAAT  
 GTTATAGCTGAATCTTGGTAACCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT  
 TTGCGCTGATGTGTTGATCATCGGTTGGATGACAGAACATAATTATGATCATGAAATAATGTTGCTTGT  
 AAAAGATTCAAGTTATTAGGAAGCTACTCTGTTTTAATCATGTTATTCATGATPACTTTAT  
 AGAACATACTGCTTCAAGGAAATATTCTTCAAAATAAGGTGTTAAACTTAACTTAACTTAACTTAACTTAACTTAACT  
 AAAA

FIG.- 45B

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CAAGAATT CGGCACGAGGGCGTGTCCAGAAAGTGTGATACTGTCAGTAGTTAATTCTCAGCTGGCAGGT  
TCCCTGAGTCAGCTGGCTCGATAGTCGTAATGAAAGAGTGTGTCAGAAAGACTTGAATGCCAGTATGAA  
TGTAGTACAGGAATTAAATTAAAGTCAGGATTCAGGACTCAAGAGGGACCTTGTGGCTCCTCTAGATTTCAAA  
TCATATTAAATTCACTCATCCACCCTAAAGTTCAGGCTTAAGGCTCAGGACTCAAGGGCTCCGGTACTTGCGAATACCTAGGGAAAGTATTTCCTG  
TGTGGAACACTCAGTAGAGCCTTAAGGCTCAGTGCATATGCAGAGTCGTGCATCCCTGCCGAACCTGATGTGGGACTTCAGAAAGT  
TGACTGCTGCGCACTCATATGCAGAGTCGTGCATCCCTGCCGAACCTGATGTGGGACTTCAGAAAGT  
ACTACGTCAGCAATTTCAGCAATTTCAGCAACAGCTGCTCGACAPGCAATATGGCAACAGGCCATTTCAGTTGCTGAGC  
ATCGGCCAAGGCCTGATGGCAAAGGCCAAGGGAGCTGGACAGAGTGAAGGAATTCAAGGCAAGCTCTTCCA  
TATCAAAGAACGCTGTGTAAGAACCTGTAGGTTGCTZAMCAGTCAGTGCATTAAGGAGTTGCGAGGCTGCTGGCAACCTT  
CACTTGACTGATGACTCCACCTGTCCTCCCTTAGGACCTGTGCAAGATCAAGAACGGGCTGCTGGCACCTT  
TACTCAAGGACATTCTGAAGGCTTCCCTTGACATCTGGCTGGCATTGTCAGATGTTGAGCTGTGTCAGAAAGGAAGGGCTT  
ATTGTTGAATTGGCCAGAATTACGACTGTCACTTCCCATTCAAGACAGCAACATGTAGAAGATGTTGAGCT  
GTGCAAGGGCTGTGCTTACAAACAGTGTGCTCCAGTCCCTCCGAGTCCCCCGGTGTCAGGATCACAGCGA  
GGAGAAAACCTCTGGAAAGTGTGGCCTCTGGCAGCAACATGATGCCCCCTGAGTACTGTGAAAAGAACGACTGTC  
AACATGCCTTATGATAACACCGATTGGTGTCTATTATGGTGACATTTGGTTAGATATTGGTATTGGTATA  
TTAAGGAAAAGATGGCTATATTCTCTTATGCAATACTTAATGTTCAAAAGAAATGCAAGATTCTGTG  
TTIAAGGCACAGGGCTGATAAGTTGGTTGGCTGCTATTGGTTTTAA  
GAGGGTTTATACTTTGTATTGAATAGTTGATGTTCACTGAGCTGAGCCAGTTGTATGTTGTGCA  
TATATGTGAACCTGTAACGTGACAAGATGAATTACTCAAGTCTCTTCTCT  
GTTGGTCCCTTCAAGTGMAMAAMAWATAGACCCCAAAAAAAAGCAATGGCGTCTGTGACGCCGAACCCGCG  
CTAATCCTGACGCTCGTGGGTGGCCCTGGCTCCTCTGAGCAGCAATGGCAATGGGAAAGGAAGAA

FIG.-46

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FIG.-48A

ATTGTTGGCCCCCTCCGAAGGCCAAGAAATTTCGGCCACCGANGGAATTTTGGTACCCAGGGG  
 GGAATGCAAATGCTGCTTCAAAACTTAGTTCTTCCATTCTCCTCCATTTCTCTAGTCTGGCCCTTGTGACACAAT  
 CTGGTAGAAAGCCGTGATAAATTGAGGGCACCTGTACCCCTCCCTGTGCCCCAGAAGGTCTCTGGAGAG  
 AAGTGCAGAAATTGTGAACACGGCGGTGGAGGGGGATGGCATTGGCTGGGGCTCCGGTATTCAGGC  
 CTGCTCACCTGCTGGAGCTTATTCTGATCTCATTTGAATGTTCCAGAGGGACATCATAAAGAGCCA  
 GAGCTCCGATTCCAAAGAGTGAATTGACATTATGAGGAGATTGGGATGGTGTGTAACATATTGATAAATACT  
 AACTTATTGTTGGGGTTCTACATAGGCAAAGAGAATTGAGGGATAGACAGTCTCCAAAGAAAAGTGAAGTGGGGAGA  
 CGTTATTCTCTAGTTCTCTAGTTCTCTAGTTCTGGCTGAGATTCTGGCTGATTTGCTGATTGTTGATTTTC  
 GAATTGGCTTTCTCTCTCTCTCTAGTTCTCTAGTTCTCTAGTTCTGGCTGAGATTCTGGCTGAGATTGAGAAGC  
 CAAATAGAFACTATTAGAGTTGACATTGACATTGACATTTAATGGGGCCATGGCTCATTTGCTGACAGCTGGCTGAC  
 TGGGTCTCCCTGCTCCAAGTCTCATGACAGGGTGTGCTGACAGCTGGGAGTCTGTGCCTCCCTCACGC  
 AGAGGCCCTAAAGCTGGACACAGAACGCCCCTAGGCTGGGCGGGATGGGACCCATGCCCTCTCTTAGA  
 GACACGGGTTCTCTGGCTTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
 TATGAGTAGTGTGTTGTGCACTTGCAAGGGTGTGCTGACTTCTAGTCTTACATCTTACATGAGGGAGTGTGATTAA  
 TGTCTGGAGTAAGCCTTACAATTAAATAGACTTTCTATCATATCCCTCATTTCTAGTCCCTTGCCAAACAAGAAATTCT  
 AAATACACACAAGCAAAAAAAATGATACTTACATGAGGAAAGGACACGTCAGGGTTTGTGCACTTCTAGTCAAA  
 TAGTTCCACTGGCCAGGATTTCCTACATAGTCAGAAACTTACACATTACTAGAGGCACACCCACCAAGGAG  
 TATTGTTGCTACTTTATCTGTCACAGGCCACAAATACCCACATTGAAAGACCCATTGTGATGGTAA  
 ACATCCCTTCTGCTTCCACAAACCCCTGTGACTGCCCTGCTGACTGCCCTGCTGCTGCTGCTGCTGCTGCTG  
 CATGAAGCAGCAAACCCAGCAAGATCTCCACCCCCCTGCTGCTCAGGACCTCTGCTGCTGCTGCTGCTGCTG  
 EGTCTCCAGGGGGCAGTGGGGCCTGTGGCAGCTGGCTGGGAGCCAGGGCTTACAGGAGGGGATGAAAGT  
 CAGTTGGGGGGCACCGTCCGGAGGAGACCTACACACCCCCACTCTACTTATCCTCCCTGCT  
 CACACACCCCTGCTGACTCTAGCAAGGGTTTATGCACTGGGATTATTTCACGAGGTGATGATGCAT  
 TTTCCTCCAGGCTGTCTAGAAAGGTGCTAAATGTTACTGTGACTTATTCTCTCAGGCACTTCAAGGATGGGG  
 TTGGTTTTGCACTTCCACTGTGCACTGGCCAGGATCCAATACGAGTCCAAATACGAGTCCAAAGGCTGACT  
 TCCCTTGTGCTGACTCTAGCAAGTGGCACTTGTGACTGCTGACTTGTGACTGCTGACTGCTGACT  
 GGCGGGCTTCTCCACCTACCCAGCCACCAAGGCCCTGACCTGCTGACTGCTGACTGCTGACT  
 CTGGCACAGCTGGAGGGTGCATGGCCCTGCTACCTTGTGACTGCTGACTGCTGACTGCTGACT  
 CTCCTCCCTGCCGTGCCCTGCCACGGGAGCCATTGTGAACTGGCT3GTGAAACGCTGATGATACCAG  
 TGGCCTCAGCCCAACCCACAGTGGAGACTGGAGACAGGGCAATGAGTCTGGTGGGGCACGTTGACATG  
 CCCATAGGGCCCCACCCAGACTTAACAGGCAGGCTTAACTGAGGCAAGGCAAGGCAACTTAACAGGCA

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AGCAAGGCCCTGCCCTCTGTGCCAGGGCCCTCTTCTGATTACACATCCCCATTTACACAGGCCCTTC  
CTTCTTAATAAAGGCTGACAGTTCTGTGGCACCCAAAGAACCCACACCAGAACAGGGAGTGAAGGGCC  
TTTGTGCCAACACTCAGCACAGCTGCGTCTGGGTGTGAGGGCATGTTCTGTGCTGGCTGGTGG  
TCTCGTGAAGACAGTTCGAGGACGGGAAATTGAGCTGTTGATCCAGTGCAGGGTGTGGGGC:GTGAGGCTTATATGTCAG  
TGCAGAGTTGCCCTGAGACGGATCTGGATATAACTATGTTAACTATGTTAAATATATC  
TGTCTGGGACCTTATCGAGTCATGAAATTGATGACTGTTGATCCAGTGCAGGGTGTGGGG  
TGTCACTCACGCTTATGACTCTTAATGTTAAAGCAGTCCATGCTTCACTGAGCCACAZC  
GATTCCCTCGAGTCCAGCCTTCTGTGCCAGTGGCTTCACTGAGCTTCACTGAGCCAC  
TGGGCTGGAGTCTCGGGCACAGTGGCCATGGGCAAGCTTAAAGAGLAGATTTC  
GCTGAAAACCCCACAGGAGATGGAGTACCTTGGCCAAAGCTTAAAGAGLAGATTTC  
GTGTGTCAGCAGGGTCAAGAACGGGATGGAAAGATGCATTCACTGAGCTTCA  
GATTAAAGATGATAAGTTCCCTGCTTAAGTTGTGCCATTGGGACTTAAAGGAGCA  
ATGATAACCAATGAGGGTTGGTTTATTATCAAACCTGAATAGCTGTGGTT  
ACTGAACATGGAGGCATTATAAGAGTGTGTTCTTAAGTTGTGTTTATTATGTA  
TGTATGTTCTTCTAAATAGTTCTCTGTGGTCTCTGTGGTTTATTATGATG  
TAACTGCAAATCAGGTGGTCTCTGTGGTCTCTGTGGTCTCTGTGGTCT  
TCGTCCACCCACCTTCAAAAATGTGAAACTGGCCCTCCCTTTGGTGA  
ACCACCTCCTACCATACTTTATGTTGAAATCTAAACTCTTGTGGTACAT  
TCGAAATAATTCTATGGCTTCCAAAAAAAGAAAAAA

FIG. - 48B

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/07044

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 G01N33/574 G01N33/50 G01N33/543 C07K16/18 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 G01N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	HÖRNER, S. ET AL.: "AC133-positive cells in the peripheral blood and bone marrow of patients with chronic myelogenous leukemia" BLOOD, vol. 92, no. 10, 15 November 1998 (1998-11-15), page 316b XP000937697 abstract	1-3,6,7, 16
A	WO 97 41224 A (AMCELL CORP) 6 November 1997 (1997-11-06) claims 28,35-41	1-3,6,7, 16
A	WO 92 15602 A (DANA FARBER CANCER INST INC) 17 September 1992 (1992-09-17) page 1, line 1 -page 3, line 13; claims 1-6	1-3,6,7, 16
		-/-

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

## \* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the International filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

8 September 2000

Date of mailing of the international search report

- 1.12.00

Name and mailing address of the ISA

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Authorized officer

Gundlach, B

## INTERNATIONAL SEARCH REPORT

national Application No

PCT/US 00/07044

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 42209 A (ICRF CLARE HALL LAB ;ARIZA RAFAEL R (GB); WOOD RICHARD D (GB); HOE) 13 November 1997 (1997-11-13) abstract; claim 22 -----	1-3,6,7, 16
A	WO 99 04030 A (KINZLER KENNETH W ;CHAN TIMOTHY A (US); MORIN PATRICE J (US); VOGE) 28 January 1999 (1999-01-28) claims 1,6,7,12,13,18,19,24,25,30,31,36 -----	1-3,6,7, 16

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 00/07044

### Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
see FURTHER INFORMATION sheet PCT/ISA/210
  
2.  Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
  
3.  Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

### Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1.  As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3.  As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-3, 6, 7, 16 (partially)

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.  
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claims 6 and 7 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

-----

Continuation of Box I.1

Rule 39.1(iv), PCT - Diagnostic method practised on the human or animal body

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
CZA8 (AC133)

2. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
BCX2

3. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
CBC2

4. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
CBC1

5. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
CBC3

6. Claims: 1-3,6,7,16 (partially), 4,5,8-10,17-22,  
25-38 (fully)

Method for screening anti colorectal cancer drugs involving  
CJA8

7. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
CJA9

8. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
CGA7

9. Claims: 1-3,6,7,16 (partially)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Method for screening anti colorectal cancer drugs involving  
BCN5

10. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
CQA1

11. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
BCN7

12. Claims: 1-3,6,7,16 (partially)

Method for screening anti colorectal cancer drugs involving  
CQA2

13. Claims: 6,7,16 (partially), 11-15,23,24 (fully)

Method for screening anti colorectal cancer drugs involving  
CAA9

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